

## BLAST Basic Local Alignment Search Tool

Job Title: lc|30069 (1209 letters)

---

•  
[Please try our new design!](#)

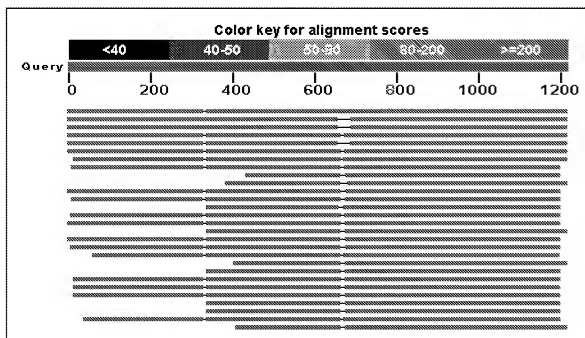
BLASTN 2.2.18+

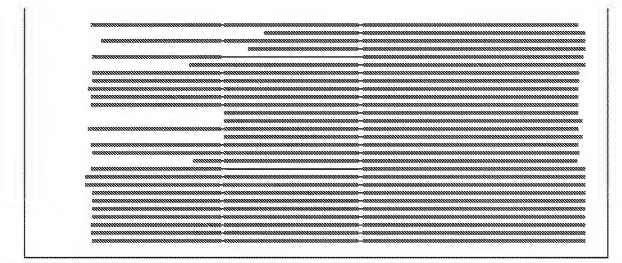
Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14. RID: D4WE0DPM01N Database: All GenBank+EMBL+DBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences) 7,426,127 sequences; 24,899,347,697 total letters

Query= Length=1209

### Distribution of 260 Blast Hits on the Query Sequence

---





Distance tree of results **NEW**

Legend for links to other resources:  UniGene  GEO  Gene  Structure 

## Sequences producing significant alignments:

(Click headers to sort columns)

EU580100.1	Mutant HIV-2 isolate VCP DeltaV3(6,6)+a-pl6 1559	2138	99%	0.0	98%
	from USA modified envelope glycoprotein (env) gene, complete cds				
EU580103.1	Mutant HIV-2 isolate VCP DeltaV1/V2/V3+a-pl6B from USA modified envelope glycoprotein (env) gene, complete cds	1122	2020	97%	0.0 97%
EU580102.1	Mutant HIV-2 isolate VCP DeltaV1/V2/V3+a-pl6A from USA modified envelope glycoprotein gene, complete cds	1122	2020	97%	0.0 97%
EU580099.1	HIV-2 isolate vcp from USA envelope glycoprotein (env) gene, complete cds	981	2151	98%	0.0 99%
EU580101.1	Mutant HIV-2 isolate VCP DeltaV3(1,1)+a-p36 920	2036	96%	0.0	98%
	from USA modified envelope glycoprotein (env) gene, complete cds				
J03654.1	Human immunodeficiency virus type 2, isolate HIV2FG	893	1995	98%	0.0 97%
U05355.1	Human immunodeficiency virus type 2 isolate HIV2CAM3, Guinea Bissau gpl60 envelope (env) gene, complete cds	632	1476	97%	1e-177 91%
U05351.1	Human immunodeficiency virus type 2 isolate HIV2CBL22 gpl60 envelope (env) gene, complete cds	617	1434	96%	3e-173 89%
AF170050.1	HIV-2 isolate 96325 from France envelope glycoprotein (env) gene, partial cds	614	884	62%	4e-172 88%
AF170042.1	HIV-2 isolate 96308 from France envelope glycoprotein (env) gene, partial cds	612	992	66%	1e-171 91%
U05352.1	Human immunodeficiency virus type 2 isolate HIV2CBL23 gpl60 envelope (env) gene, complete cds	599	1497	97%	1e-167 93%
DQ213030.1	HIV-2 isolate P2-1996 from Sweden envelope glycoprotein (env) gene, partial cds	597	1347	96%	4e-167 87%
AF170047.1	HIV-2 isolate 96330 from France envelope glycoprotein (env) gene, partial cds	597	973	69%	4e-167 87%
U05350.1	Human immunodeficiency virus type 2 isolate HIV2CBL21 gpl60 envelope (env) gene, complete cds	595	1380	96%	1e-166 89%
AY509259.1	HIV-2 isolate MCN13, complete genome	593	1486	97%	5e-166 93%
AJ001162.1	Human Immunodeficiency Virus Type 2 partial envelope sequence, isolate sar from child in vertical transmission case	590	1041	71%	6e-165 91%
AY509260.1	HIV-2 isolate MCR35, complete genome	588	1480	97%	2e-164 93%
L25445.1	Human immunodeficiency virus type 2 proviral envelope glycoprotein (env) gene, complete cds	586	1414	96%	8e-164 90%
AY168925.1	HIV-2 isolate MIC97 envelope glycoprotein (env) gene, partial cds	582	1347	92%	1e-162 91%

AF176768.1	HIV-2 isolate SS2 from Spain envelope glycoprotein (env) gene, partial cds	582	905	65%	1e-162	89%
DQ400384.1	HIV-2 isolate CalHIV-2(BD) from India nonfunctional envelope glycoprotein (env) gene, partial sequence	580	982	69%	4e-162	88%
AJ238998.1	Human immunodeficiency virus type 2, env gene for envelope glycoprotein precursor gp130, cell line HVS T-cell CB23 (late)	580	1445	95%	4e-162	91%
AJ238996.1	Human immunodeficiency virus type 2, env gene for envelope glycoprotein precursor gp160, cell line Molt4.c8 (late)	580	1445	95%	4e-162	91%
AJ238995.1	Human immunodeficiency virus type 2, env gene for envelope glycoprotein precursor gp160, cell line Molt4.c8(early)	580	1445	95%	4e-162	91%
M31113.1	Human immunodeficiency virus type 2 (HIV-2), complete proviral genome	580	982	69%	4e-162	88%
M86924.1	Human immunodeficiency virus type 2 (ST/24.1C#2) envelope glycoprotein (env) gene, 5'end	580	971	69%	4e-162	88%
M30895.1	Human immunodeficiency virus type 2 (isolate GH-1) proviral DNA complete genome, clone 8	580	1329	94%	4e-162	89%
AF176770.1	HIV-2 isolate SS4 from Spain envelope glycoprotein (env) gene, partial cds	577	936	65%	5e-161	92%
AJ238997.1	Human immunodeficiency virus type 2 env gene for envelope glycoprotein precursor gp160, cell line HVS T-cell CB23 (early)	575	1440	95%	2e-160	91%
AF170044.1	HIV-2 isolate 96327 from France envelope glycoprotein (env) gene, partial cds	575	857	63%	2e-160	89%
L36874.1	HIV-2 isolate 7312a clone JK, partial genome	573	1236	95%	6e-160	89%
AF176769.1	HIV-2 isolate SS3 from Spain envelope glycoprotein (env) gene, partial cds	573	949	66%	6e-160	92%
DQ870442.1	HIV-2 clone NARI-H2-5.4 from India envelope glycoprotein (env) gene, partial cds	571	953	69%	2e-159	88%
AF170049.1	HIV-2 isolate 96203 from France envelope glycoprotein (env) gene, partial cds	571	1065	78%	2e-159	88%
DQ870450.1	HIV-2 clone NARI-H2-7.7 from India envelope glycoprotein (env) gene, partial cds	569	1373	95%	8e-159	90%
DQ870449.1	HIV-2 clone NARI-H2-7.5 from India envelope glycoprotein (env) gene, partial cds	569	1379	95%	8e-159	90%
DQ400382.1	HIV-2 isolate Cal3HIV-2(818) from India nonfunctional envelope glycoprotein (env) gene, partial sequence	569	1419	96%	8e-159	92%
AJ239000.1	Human immunodeficiency virus type 2, env gene for envelope glycoprotein precursor gp160, cell line HVS T-cell Kesting (late)	569	1428	95%	8e-159	91%
AJ238999.1	Human immunodeficiency virus type 2, env gene for envelope glycoprotein precursor gp160, cell line HVS T-cell Kesting (early)	569	1434	95%	8e-159	91%
AF170032.1	HIV-2 isolate 96323 from France envelope glycoprotein (env) gene, partial cds	569	999	69%	8e-159	90%
AJ001163.1	Human Immunodeficiency Virus Type 2 partial envelope sequence, isolate arm from mother in vertical transmission case	569	1010	70%	8e-159	91%

AF082339.1	HIV-2 isolate ALI from Guinea-Bissau, complete genome	569	1419	96%	8e-159	92%
L76739.1	Human immunodeficiency virus type 2 (HIV-2 ARM) proviral surface glycoprotein (gp125) gene, partial cds	569	1010	70%	8e-159	91%
U05353.1	Human immunodeficiency virus type 2 isolate HIV2CBL24 gp160 envelope (env) gene, complete cds	569	1428	95%	8e-159	91%
DQ870448.1	HIV-2 clone NARI-H2-7.2 from India envelope glycoprotein (env) gene, partial cds	564	1368	95%	4e-157	90%
AF170040.1	HIV-2 isolate 96202 from France envelope glycoprotein (env) gene, partial cds	564	1052	75%	4e-157	94%
U05359.1	Human immunodeficiency virus type 2 isolate HIV2CAM1, Guinea Bissau gp160 envelope (env) gene, complete cds	564	995	70%	4e-157	91%
DQ213034.1	HIV-2 isolate P4-2000 from Sweden envelope glycoprotein (env) gene, partial cds	562	1410	98%	1e-156	90%
DQ213033.1	HIV-2 isolate P4-1992 from Sweden envelope glycoprotein (env) gene, partial cds	558	1428	98%	2e-155	92%
DQ870471.1	HIV-2 clone NARI-H2-14.6 from India envelope glycoprotein (env) gene, partial cds	556	1408	96%	6e-155	91%
DQ870470.1	HIV-2 clone NARI-H2-14.5 from India envelope glycoprotein (env) gene, partial cds	556	1397	96%	6e-155	90%
DQ870469.1	HIV-2 clone NARI-H2-14.2 from India envelope glycoprotein (env) gene, partial cds	556	1392	96%	6e-155	90%
Z48731.1	Human immunodeficiency virus type 2 gag, pol, vif, vpx, vpr, tat, rev, nef and env genes	556	1392	97%	6e-155	90%
D00835.1	Human immunodeficiency virus 2 proviral DNA, complete genome	556	1412	97%	6e-155	90%
U05354.1	Human immunodeficiency virus type 2 isolate HIV2CAM2, Guinea Bissau gp160 envelope (env) gene, complete cds	556	1423	97%	6e-155	91%
U07106.1	Human immunodeficiency virus type 2 hiv2d766 envelope protein gp105 (env) gene, partial cds	556	1272	97%	6e-155	90%
DQ213036.1	HIV-2 isolate P4-2002 from Sweden envelope glycoprotein (env) gene, partial cds	555	1340	98%	2e-154	91%
U07104.1	Human immunodeficiency virus type 2 hiv2d1024 envelope protein gp105 (env) gene, partial cds	555	1353	96%	2e-154	90%
AY249822.1	HIV-2 subject DKN142 from Senegal envelope glycoprotein (env) gene, partial cds	551	551	39%	3e-153	87%
X05291.1	Human immunodeficiency virus type 2 ROD isolate RNA genome (HIV-2)	551	980	71%	3e-153	90%
AF176767.1	HIV-2 isolate SS1 from Spain envelope glycoprotein (env) gene, partial cds	551	953	66%	3e-153	93%
M15390.1	Human immunodeficiency virus type 2, isolate ROD, complete proviral genome	551	980	71%	3e-153	90%
DQ870477.1	HIV-2 clone NARI-H2-16.6 from India envelope glycoprotein (env) gene, partial cds	549	1379	96%	1e-152	92%

DQ870476.1	HIV-2 clone NARI-H2-16.5 from India envelope glycoprotein (env) gene, partial cds	549	1323	96%	1e- 152	89%
DQ870475.1	HIV-2 clone NARI-H2-16.4 from India envelope glycoprotein (env) gene, partial cds	549	1323	96%	1e- 152	89%
AF170045.1	HIV-2 isolate 96329 from France envelope glycoprotein (env) gene, partial cds	547	949	69%	4e- 152	88%
DQ213029.1	HIV-2 isolate P2-1994 from Sweden envelope glycoprotein (env) gene, partial cds	545	1288	96%	1e- 151	88%
J04498.1	Human immunodeficiency virus type 2, isolate SBLISY, complete genome	545	1327	96%	1e- 151	89%
DQ870468.1	HIV-2 clone NARI-H2-13.2 from India envelope glycoprotein (env) gene, partial cds	542	1371	95%	2e- 150	90%
DQ870467.1	HIV-2 clone NARI-H2-13.1 from India envelope glycoprotein (env) gene, partial cds	542	1364	95%	2e- 150	90%
DQ870466.1	HIV-2 clone NARI-H2-13.3 from India envelope glycoprotein (env) gene, partial cds	542	1358	95%	2e- 150	90%
DQ870465.1	HIV-2 clone NARI-H2-12.1 from India envelope glycoprotein (env) gene, partial cds	542	1279	96%	2e- 150	88%
DQ870464.1	HIV-2 clone NARI-H2-12.4 from India envelope glycoprotein (env) gene, partial cds	542	1268	96%	2e- 150	87%
DQ870463.1	HIV-2 clone NARI-H2-12.3 from India envelope glycoprotein (env) gene, partial cds	542	1279	96%	2e- 150	88%
AY249826.1	HIV-2 subject MBN5 from Senegal envelope glycoprotein (env) gene, partial cds	540	540	38%	6e- 150	87%
U05358.1	Human immunodeficiency virus type 2 isolate HIV2CAM6, Guinea Bissau gpl60 envelope (env) gene, complete cds	540	1456	96%	6e- 150	92%
AF170035.1	HIV-2 isolate 96201 from France envelope glycoprotein (env) gene, partial cds	536	964	67%	8e- 149	90%
DQ870447.1	HIV-2 clone NARI-H2-6.1 from India envelope glycoprotein (env) gene, partial cds	532	1331	96%	1e- 147	89%
DQ213031.1	HIV-2 isolate P2-1998 from Sweden envelope glycoprotein (env) gene, partial cds	532	1264	96%	1e- 147	87%
DQ870452.1	HIV-2 clone NARI-H2-8.4 from India envelope glycoprotein (env) gene, partial cds	531	1297	96%	4e- 147	88%
DQ870432.1	HIV-2 clone NARI-H2-1.5 from India envelope glycoprotein (env) gene, partial cds	531	966	70%	4e- 147	91%
DQ870431.1	HIV-2 clone NARI-H2-1.1 from India envelope glycoprotein (env) gene, partial cds	531	966	70%	4e- 147	91%
DQ870430.1	HIV-2 clone NARI-H2-1.4 from India envelope glycoprotein (env) gene, partial cds	531	932	70%	4e- 147	89%
DQ213035.1	HIV-2 isolate P4-2001 from Sweden envelope glycoprotein (env) gene, partial cds	529	910	71%	1e- 146	87%
AF170037.1	HIV-2 isolate 96152 from France envelope glycoprotein (env) gene, partial cds	527	875	63%	5e- 146	91%
DQ870483.1	HIV-2 clone NARI-H2-18.6 from India envelope glycoprotein (env) gene, partial cds	525	1342	96%	2e- 145	89%

cds						
DQ870482.1	HIV-2 clone NARI-H2-18.1 from India envelope glycoprotein (env) gene, partial cds	525	1342	96%	2e- 145	89%
DQ870481.1	HIV-2 clone NARI-H2-18.4 from India envelope glycoprotein (env) gene, partial cds	525	1342	96%	2e- 145	89%
DQ870441.1	HIV-2 clone NARI-H2-4.1 from India envelope glycoprotein (env) gene, partial cds	525	962	68%	2e- 145	92%
DQ870440.1	HIV-2 clone NARI-H2-4.4 from India envelope glycoprotein (env) gene, partial cds	525	962	68%	2e- 145	92%
DQ870439.1	HIV-2 clone NARI-H2-4.3 from India envelope glycoprotein (env) gene, partial cds	525	962	68%	2e- 145	92%
DQ400383.1	HIV-2 isolate Cal4HIV-2(889) from India nonfunctional envelope glycoprotein (env) gene, partial sequence	525	921	68%	2e- 145	89%
U22047.1	Human immunodeficiency virus type 2, complete genome	525	1384	96%	2e- 145	91%
DQ870480.1	HIV-2 clone NARI-H2-17.6 from India envelope glycoprotein (env) gene, partial cds	523	1316	96%	6e- 145	90%
DQ870479.1	HIV-2 clone NARI-H2-17.5 from India envelope glycoprotein (env) gene, partial cds	523	1316	96%	6e- 145	90%
DQ870478.1	HIV-2 clone NARI-H2-17.2 from India envelope glycoprotein (env) gene, partial cds	523	1316	96%	6e- 145	90%
U07108.1	Human immunodeficiency virus type 2 hiv2d868 envelope protein gp105 (env) gene, partial cds	523	1342	95%	6e- 145	91%
DQ870446.1	HIV-2 clone NARI-H2-6.4 from India envelope glycoprotein (env) gene, partial cds	521	1316	95%	2e- 144	90%
DQ870445.1	HIV-2 clone NARI-H2-6.3 from India envelope glycoprotein (env) gene, partial cds	521	1320	96%	2e- 144	89%
DQ870444.1	HIV-2 clone NARI-H2-5.2 from India envelope glycoprotein (env) gene, partial cds	521	903	69%	2e- 144	88%

## Alignments

>gb|EU580100.1| Mutant HIV-2 isolate VCP DeltaV3(6,6)+a-p16 from USA modified envelope glycoprotein (env) gene, complete cds  
Length=2172

Sort alignments for this  
E value Score Percen  
Query start position

Score = 1559 bits (844), Expect = 0.0  
Identities = 864/874 (98%), Gaps = 0/874 (0%)  
Strand=Plus/Plus

Query	336	CCATTGCAATACATCAGTCATCAAAGAGTCATGTGATAAGCACTATTGGGATGCTATGAG	395
Sbjct	582	CCATTGCAATACATCAGTCATCACAGAGTCATGTGATAAGCACTATTGGGATGCTATGAG	641
Query	396	GTTTAGATACTGTGCACCACCGGGTTTTGCCCTACTAAGATGCAATGATATTAATTATTC	455
Sbjct	642	GTTTAGATACTGTGCACCACCGGGTTTTGCCCTACTAAGATGCAATGATACTAATTATTC	701
Query	456	AGGCTTTGCACCTAATTGCTCTAAAGTAGTAGCTGCTACATGCCAGAAATGATGGAAAC	515
Sbjct	702	AGGCTTTGCACCTAATTGCTCTAAAGTAGTAGCTGCTACATGCCAGAAATGATGGAAAC	761
Query	516	GCAATCTTCTACATGGTTTGGCTTTAATGGCACTAGAACAGAAAAAGAACATATATCTA	575
Sbjct	762	GCAATCTTCTACATGGTTTGGATTTAATGGCACTAGAGCAGAAAAAGAACATATATATA	821
Query	576	TTGGCATGGTAAAAATAACAGAACTATTATCAGCTTAAATAACTTTTATAATCTCAGCAT	635
Sbjct	822	TTGGCATGGTAAAAATAACAGAACTATTATCAGCTTAAATAACTTTTATAATCTCAGCAT	881
Query	636	GCATTGTAAGAGGCCGGGAAATAAGGGTGCCGGCAAAACCCAGGCAAGCATGGTGTGGTT	695
Sbjct	882	GCATTGTAAGAGGCCGGGAAATAAGGGTGCCGGCAAAACCCAGGCAAGCATGGTGTGGTT	941
Query	696	CAAAGGCCAATGGAAGGAAGCCATGCAGGAGGTGAAGGAGACCCCTTGCGAAACATCCAG	755
Sbjct	942	CAAAGGCCAATGGAAGGAAGCCATGCAGGAGGTGAAGGAGACCCCTTGCGAAACATCCAG	1001
Query	756	ATATAAGGGAACAGGAGCCGCACAGAGAATATTAAATTTAAAGCACCAGGAAGAGGCTC	815
Sbjct	1002	ATATAAGGGAACAGGAGCCGCACAGAGAATATTAAATTTAAAGCACCAGGAAGAGGCTC	1061
Query	816	AGACCCAGAAGCAGCATACATGTGGACTAACTGCAGAGGGGAATTTCTCTACTGCGACAT	875
Sbjct	1062	AGACCCAGAAGCAGCATACATGTGGACTAACTGCAGAGGGGAATTTCTCTACTGCAACAT	1121
Query	876	GACTTGGTTTCCCTCAATTGGGTAGATAACAGGACGGGTGAGAAACAGCGCAATTATGCACC	935
Sbjct	1122	GGCTTGGTTTCCCTCAATTGGGTAGAAAAACAGGACGGGTGAGAAACAGCGCAATTATGCACC	1181
Query	936	GTGCCATATAAGACAAATAATTAATACTTGGCACAGGGTAGGGAAAAACGTATATTGGC	995
Sbjct	1182	GTGCCATATAAGGCAAAATAATTAATACTTGGCACAGGGTAGGGAAAAACATATATTGGC	1241



```

Query 996 TCCCAGGGAAGGGGAGTTGACCTGCAACTCAACAGTGACCAGCATAATTGCCAACATTGA 1055
          |||
Sbjct 1242 TCCCAGGGAAGGGGAGTTGACCTGCAACTCAACAGTGACCAGCATAATTGCCAACATTGA 1301
          |||

Query 1056 TACGGGAGATCAACAGATATTACCTTTAGTGAGAGGTGGCAGAACTATACCGATTGGA 1115
          |||
Sbjct 1302 TACGGGAGATCAACAGATATTACCTTTAGTGAGAGGTGGCAGAACTATACCGATTGGA 1361
          |||

Query 1116 ATTGGGAGATTACAAATTTAGTAGAAATCACACCAATTGGCTTCGCACCTACATCAGTAAA 1175
          |||
Sbjct 1362 ATTGGGAGATTACAAATTTAGTAGAAATCACACCAATTGGCTTCGCACCTACATCAGTAAA 1421
          |||

Query 1176 GAGATACTCCTCTGCTCACCAGAGACATACAAGA 1209
          |||
Sbjct 1422 GAGATACTCCTCTGCTCACCAGAGACATACAAGA 1455
          |||

```

Score = 579 bits (313), Expect = 1e-161  
 Identities = 323/328 (98%), Gaps = 0/328 (0%)  
 Strand=Plus/Plus

```

Query 1 ATGAAGGGTAGTAAGAATCAACTGCTGATTGCTATTGTACTAGCTAGTGCTTACCTAACA 60
          |||
Sbjct 1 ATGAAGGGTAGTAAGAATCAACTGCTGATTGCTATTGTACTAGCTAGTGCTTACCTAACA 60
          |||

Query 61 CATTGCAAGCAATTTGTGACTGTTTTCTATGGCATAACCCGCGTGGAGGAATGCATCCATT 120
          |||
Sbjct 61 CATTGCAAGCAATTTGTGACTGTTTTCTATGGCATAACCCGCGTGGAGGAATGCATCCATT 120
          |||

Query 121 CCCCTGTTTTTGTGCAACCAAAAATAGAGATACTTGGGGAACGTACAGTGCTTGCACAGAC 180
          |||
Sbjct 121 CCCCTGTTTTTGTGCAACCAAAAATAGAGATACTTGGGGAACCATACAGTGCTTGCACAGAC 180
          |||

Query 181 AATGATGATTATCAGGAAATAGCTTTAAATGTAACAGAGGCTTTCGATGCATGGGATAAT 240
          |||
Sbjct 181 AATGATGATTATCAGGAAATAGCTTTAAATGTAACAGAGGCTTTCGATGCATGGGATAAT 240
          |||

Query 241 ACAGTAACAGAAACAAGCAGTGGAGGATGTCTGGAATCTATTTGAGACATCAATAAAACCA 300
          |||
Sbjct 241 ACAGTAACAGAAACAAGCAGTGGAGGATGTCTGGAATCTATTTGAGACATCAATAAAACCA 300
          |||

Query 301 TGTGTCAAATTAACACCCCTTATGTGTAG 328
          |||
Sbjct 301 TGTGTCAAATTAACACCCCTTATGTGTAG 328
          |||

```

>gb|EU580103.1| Mutant HIV-2 isolate VCP DeltaV1/V2/V3+a-pl6B from USA modified  
 envelope glycoprotein (env) gene, complete cds  
 Length=1896

Sort alignments for this  
 E value Score Perce  
 Query start position

Score = 1122 bits (607), Expect = 0.0  
 Identities = 639/654 (97%), Gaps = 3/654 (0%)  
 Strand=Plus/Plus

```

Query 1 ATGAAGGGTAGTAAGAATCAACTGCTGATTGCTATTGTACTAGCTAGTGCTTACCTAACA 60
          |||
Sbjct 1 ATGAAGGGTAGTAAGAATCAACTGCTGATTGCTATTGTACTAGCTAGTGCTTACCTAACA 60
          |||

Query 61 CATTGCAAGCAATTTGTGACTGTTTTCTATGGCATAACCCGCGTGGAGGAATGCATCCATT 120
          |||
Sbjct 61 CATTGCAAGCAATTTGTGACTGTTTTCTATGGCATAACCCGCGTGGAGGAATGCATCCATT 120
          |||

Query 121 CCCCTGTTTTTGTGCAACCAAAAATAGAGATACTTGGGGAACGTACAGTGCTTGCACAGAC 180
          |||
Sbjct 121 CCCCTGTTTTTGTGCAACCAAAAATAGAGATACTTGGGGAACACACAGTGCTTGCACAGAC 180
          |||

Query 181 AATGATGATTATCAGGAAATAGCTTTAAATGTAACAGAGGCTTTCGATGCATGGGATAAT 240
          |||
Sbjct 181 AATGATGATTATCAGGAAATAGCTTTAAATGTAACAGAGGCTTTCGATGCATGGGATAAT 240
          |||

Query 241 ACAGTAACAGAAACAAGCAGTGGAGGATGTCTGGAATCTATTTGAGACATCAATAAAACCA 300
          |||

```

Score = 898 bits (486), Expect = 0.0  
Identities = 512/525 (97%), Gaps = 0/525 (0%)  
Strand=Plus/Plus

>gb|EU580102.1| Mutant HIV-2 isolate VCP DeltaV1/V2/V3+a-pl6A from USA modified envelope glycoprotein gene, complete cds  
Length=1896

9/18/2008

Score = 1122 bits (607), Expect = 0.0  
 Identities = 639/654 (97%), Gaps = 3/654 (0%)  
 Strand=Plus/Plus

```

Query 1 ATGAAGGGTAGTAAAGATCAACTGCTGATTGCTATTGTACTAGCTAGTGCTTACCTAACA 60
Sbjct 1 ATGAAGGGTAGTAAAGATCAACTGCTGATTGCTATTATACTAGCTAGTGCTTACCTAACA 60

Query 61 CATTGCAAGCAATTTGTGACTGTTTTCTATGGCATAACCCGCGTGAGGAATGCATCCATT 120
Sbjct 61 CATTGCAAGCAATTTGTGACTGTTTTCTATGGCATAACCCGCGTGAGGAATGCATCCATT 120

Query 121 CCCCTGTTTTGTGCAACCAAAATAGAGATACTTTGGGGAACGTACAGTGCTTGCACAGAC 180
Sbjct 121 CCCCTGTTTTGTGCAACCAAAATAGAGATACTTTGGGGAACACACAGTGCTTGCACAGAC 180

Query 181 AATGATGATTATCAGGAAATAGCTTTAAATGTAACAGAGGCTTCGATGCATGGGATAAT 240
Sbjct 181 AATGATGATTATCAGGAAATAGCTCTAAATGTAACAGAGGCTTCGATGCATGGAATAAT 240

Query 241 ACAGTAACAGAACAGCAGTGAGGATGCTGGAATCTATTTGAGACATCAATAAAACCA 300
Sbjct 241 ACAGTAACAGAACAGCAGTGAGGATGCTGGAATCTATTTGAGACATCAATAAAACCA 300

Query 301 TGTGTCAAATTAACACCCTTATGTGTAGTGCCCGCCATTGCAATACATCAGTCATCA-A 359
Sbjct 301 TGTGTCAAATTAACACCCTTATGTGTAGTGCCCGCCATTGCAATACATCAGTCATCA 360

Query 360 AGAGTCATGTGATAAGCACTATTGGGATGCTATGAGGTTTAGATACTGTGCACCACCGGG 419
Sbjct 361 A-AGTCATGTGATAAGCACTATTGGGATGCTATGAGGTTTAGATACTGTGCACCACCGGG 419

Query 420 TTTTGCCCTACTAAGATGCAATGATATTAATTATTACAGGCTTGCACCTAATTGCTCTAA 479
Sbjct 420 TTTTGCCCTACTAAGATGCAATGATATTAATTATTACAGGCTTGCACCTAATTGCTCTAA 479

Query 480 AGTAGTAGCTGTACATGCACCAGAAATGATGAAACGCAATCTTCTACATGGTTTGGCTT 539
Sbjct 480 AGTAGTAGCTGTACATGCACCAGAAATGATGAAACGCAATCTTCTACATGGTTTGGATT 539

Query 540 TAATGGCAGTACAGCAGAAAAATAGAACATATATCTATTGGCATGGTAAAAATAACAGAAC 599
Sbjct 540 TAATGGCAGTACAGCAGAAAAATAGAACATATATATATTGGCATGGTAAAGATAACAGAAC 599

Query 600 TATTATCAGCTTAAATAACTTTTATAATCTCACTATGCATTGTAAGAG-GCCGG 652
Sbjct 600 TATTATCAGCTTAAATAACTTTTATAATCTCACTATGCATTGTAAGGGTGCCGG 653

```

Score = 898 bits (486), Expect = 0.0  
 Identities = 512/525 (97%), Gaps = 0/525 (0%)  
 Strand=Plus/Plus

```

Query 685 TGGTGTGGTTCAAAGGCGAATGGAAGGAAGCCATGCAGGAGGTGAAGGAGACCCCTTGGC 744
Sbjct 685 TGGTGTGGTTCAAAGGCGAATGGAAGGAAGCCATGCAGGAGGTGAAGGAGACCCCTTGGC 714

Query 745 AAACATCCAGATATAAAGGGAACAGGAGCCGCACAGAGAATATTAAATTTAAAGCACCA 804
Sbjct 715 AAACATCCAGATATAAAGGGAACAGGAGCCGCACAGAGAATATTAAATTTAAAGCACCA 774

Query 805 GGAAGAGGCTCAGACCCAGAACGAGCAGATACATGTGGACTAACTGCAGAGGGGAAATTTCTC 864
Sbjct 775 GGAAGAGGCTCAGACCCAGAACGAGCAGATACATGTGGACTAACTGCAGAGGGGAAATTTCTC 834

Query 865 TACTGCGACATGACTTGGTTCCTCAATTGGGTAGATAACAGGACGGGTGAGAAACAGCGC 924
Sbjct 835 TACTGCAACATGGCTTGGTTCCTCAATTGGGTAGAAACAGGACGGGTGAGAAACAGCGC 894

Query 925 AATTATGCACCGTGCCATATAAGACAAATAAATAACTTTGGCACAGGGTAGGGAAAAAC 984
Sbjct 895 AATTATGCACCGTGCCATATAAGGCAAAAAATAAATAACTTTGGCACAGGGTAGGGAAAAAC 954

Query 985 GTATATTTCGCTCCAGGGGAAGGGAGTTGACCTGCAACTCAACAGTGACCAAGCATTAAT 1044

```

Sbjct	955	ATATATTGCTCCCGAGGGAAGGAGTGTTTACCTGCAACTCAACAGTGACCAGCATAATT	1014
Query	1045	GCCAAACATTGATACGGGAGATCAACAGATATTACCTTTAGTGAGAGGTGGCAGAACTA	1104
Sbjct	1015	GCCAAACATTGATACGGGAGATCAACAGATATTACCTTTAGTGAGAGGTGGCAGAACTA	1074
Query	1105	TACCGATTGGAATTGGGAGATTACAAATTAGTAGAAATCACACCAATTGGCTTCGCACCT	1164
Sbjct	1075	TACCGATTGGAATTGGGAGATTACAAATTAGTAGAAATCACACCAATTGGCTTCGCACCT	1134
Query	1165	ACATCAGTAAAGAGATACTCCTCTGCTCACCAGAGACATACAAGA	1209
Sbjct	1135	ACATCAGTAAAGAGATACTCCTCTGCTCACCAGAGACATACAAGA	1179

>gb|EU580099.1| HIV-2 isolate vcp from USA envelope glycoprotein (env) gene,  
complete cds  
Length=2220

Sort alignments for this  
E value Score Percen  
Query start position

Score = 981 bits (531), Expect = 0.0  
Identities = 537/540 (99%), Gaps = 0/540 (0%)  
Strand=Plus/Plus

Query	670	AAACCCAGGCAAGCATGGTGTGGTTCAAAGGCGAATGGAAGGAAGCCATGCAGGAGGTG	729
Sbjct	964	AAACCCAGGCAAGCATGGTGTGGTTCAAAGGCGAATGGAAGGAAGCCATGCAGGAGGTG	1023
Query	730	AAGGAGACCCCTTGGCAAAACATCCAGATATAAAGGGAAACAGGAGCCGCACAGAGAATATT	789
Sbjct	1024	AAGGAGACCCCTTGGCAAAACATCCAGATATAAAGGGAAACAGGAGCCGCACAGAGAATATT	1083
Query	790	AAATTTAAAGCACAGGAAGAGGCTCAGACCCAGAAAGCAGATACATGTGGACTAACTGC	849
Sbjct	1084	AAATTTAAAGCACAGGAAGAGGCTCAGACCCAGAAAGCAGATACATGTGGACTAACTGC	1143
Query	850	AGAGGGGAATTTCTCTACTGCGACATGACTTGGTTCCTCAATTGGGTAGATAACAGGACG	909
Sbjct	1144	AGAGGGGAATTTCTCTACTGCAACATGACTTGGTTCCTCAATTGGGTAGAAAACAGGACG	1203
Query	910	GGTCAGAAACAGCGCAATTATGCACCGTGCATATAAGACAAATAATTAATCTTGGCAC	969
Sbjct	1204	GGTCAGAAACAGCGCAATTATGCACCGTGCATATAAGGCAATAATTAATCTTGGCAC	1263
Query	970	AGGGTAGGGGAAAACGTATATTGGCTCCCGAGGGAAGGGGAGTTGACCTGCAACTCAACA	1029
Sbjct	1264	AGGGTAGGGGAAAACGTATATTGGCTCCCGAGGGAAGGGGAGTTGACCTGCAACTCAACA	1323
Query	1030	GTGACCAGCATAAATGCCAACATTGATACGGGAGATCAACAGATATTACCTTTAGTGCA	1089
Sbjct	1324	GTGACCAGCATAAATGCCAACATTGATACGGGAGATCAACAGATATTACCTTTAGTGCA	1383
Query	1090	GAGGTGGCAGAACTATACCGATTGGAATTGGGAGATTACAAATTAGTAGAAATCACACCA	1149
Sbjct	1384	GAGGTGGCAGAACTATACCGATTGGAATTGGGAGATTACAAATTAGTAGAAATCACACCA	1443
Query	1150	ATTGGCTTCGCACCTACATCAGTAAAGAGATACTCCTCTGCTCACCAGAGACATACAAGA	1209
Sbjct	1444	ATTGGCTTCGCACCTACATCAGTAAAGAGATACTCCTCTGCTCACCAGAGACATACAAGA	1503

Score = 584 bits (316), Expect = 3e-163  
Identities = 324/328 (98%), Gaps = 0/328 (0%)  
Strand=Plus/Plus

Query	1	ATGAAGGGTAGTAAGAATCAACTGCTGATTGCTATTGTACTAGCTAGTGCTTACCTAACA	60
Sbjct	1	ATGAAGGGTAGTAAGAATCAACTGCTGATTGCTATTGTACTAGCTAGTGCTTACCTAACA	60
Query	61	CATTGCAAGCAATTTGTGACTGTTTTCTATGGCATAACCCGCTGGAGGAATGCATCCATT	120
Sbjct	61	CATTGCAAGCAATTTGTGACTGTTTTCTATGGCATAACCCGCTGGAGGAATGCATCCATT	120

```

Query 121 CCCCTGTTTTTGTGCAACCAAAATAGAGATACTTGGGGAACGTGTACAGTGCTTGCCAGAC 180
      |||
Sbjct 121 CCCCTGTTTTTGTGCAACCAAAATAGAGATACTTGGGGAACCATACAGTGCTTGCCAGAC 180

Query 181 AATGATGATTATCAGGAAATAGCTTTAAATGTAACAGAGGCTTCGATGCATGGGATAAT 240
      |||
Sbjct 181 AATGATGATTATCAGGAAATAGCTTTAAATGTAACAGAGGCTTCGATGCATGGGATAAT 240

Query 241 ACAGTAACAGAAACAAGCAGTGGAGGATGTCTGGAATCTATTTGAGACATCAATAAAACCA 300
      |||
Sbjct 241 ACAGTAACAGAAACAAGCAGTGGAGGATGTCTGGAATCTATTTGAGACATCAATAAAACCA 300

Query 301 TGTGTCAAATTAACACCCCTTATGTGTAG 328
      |||
Sbjct 301 TGTGTCAAATTAACACCCCTTATGTGTAG 328

```

Score = 584 bits (316), Expect = 3e-163  
 Identities = 322/325 (99%), Gaps = 0/325 (0%)  
 Strand=Plus/Plus

```

Query 336 CCATTGCAATACATCAGTCATCAAGAGTCATGTGATAAGCACTATTGGGATGCTATGAG 395
      |||
Sbjct 582 CCATTGCAATACATCAGTCATCAGAGTCATGTGATAAGCACTATTGGGATGCTATGAG 641

Query 396 GTTTAGATACTGTGCCACCACCGGTTTTTGCCCTACTAAGATGCAATGATATTAATTATTC 455
      |||
Sbjct 642 GTTTAGATACTGTGCCACCACCGGTTTTTGCCCTACTAAGATGCAATGATATTAATTATTC 701

Query 456 AGGCTTTGCACCTAATTGCTCTAAAGTAGTAGCTGTACATGCACCAAGATGATGGAAC 515
      |||
Sbjct 702 AGGCTTTGCACCTAATTGCTCTAAAGTAGTAGCTGTACATGCACCAAGATGATGGAAC 761

Query 516 GCAATCTTCTACATGGTTTGGCTTTAATGGCACTAGAACAGAAAATAGAACATATATCTA 575
      |||
Sbjct 762 GCAATCTTCTACATGGTTTGGCTTTAATGGCACTAGAACAGAAAATAGAACATATATCTA 821

Query 576 TTGGCATGGTAAAAATAACAGAACTATTATCAGCTTAAATAACTTTTATAATCTCACTAT 635
      |||
Sbjct 822 TTGGCATGGTAAAAATAACAGAACTATTATCAGCTTAAATAACTTTTATAATCTCACTAT 881

Query 636 GCATTGTAAGAGGCCGGGAATAAG 660
      |||
Sbjct 882 GCATTGTAAGAGGCCGGGAATAAG 906

```

>gb|EU580101.1| Mutant HIV-2 isolate VCP DeltaV3(1,1)+a-p36 from USA modified  
 envelope glycoprotein (env) gene, complete cds  
 Length=2142

Sort alignments for this  
 E value Score Percen  
 Query start position

Score = 920 bits (498), Expect = 0.0  
 Identities = 516/525 (98%), Gaps = 0/525 (0%)  
 Strand=Plus/Plus

```

Query 685 TGGTGTGGTTCAAAGGCGAATGGAAGGAAGCCATGCAGGAGGTGAAGGAGACCCCTTGGC 744
      |||
Sbjct 901 TGGTGTGGTTCAAAGGCGAATGGAAGGAAGCCATGCAGGAGGTGAAGGAGACCCCTTGGC 960

Query 745 AAACATCCAGATATATAAGGGAACAGGAGCCGCACAGAGAATATTAAATTTAAAGCACCA 804
      |||
Sbjct 961 AAACATCCAGATATATAAGGGAACAGGAGCCGCACAGAGAATATTAAATTTAAAGCACCA 1020

Query 805 GGAAGAGGGCTCAGACCCAGAAGCAGCATACATGTGGACTAACTGCAGAGGGGAATTTCTC 864
      |||
Sbjct 1021 GGAAGAGGGCTCAGACCCAGAAGCAGCATACATGTGGACTAACTGCAGAGGGGAATTTCTC 1080

Query 865 TACTGCGACATGACTTGGTTCTCAATTGGGTAGATAACAGGACGGGTGAGAAACAGCGC 924
      |||
Sbjct 1081 TACTGCAACATGGCTTGGTTCTCAATTGGGTAGAAAAACAGGACGGGTGAGAAACAGCGC 1140

Query 925 AATTATGCACCGTGCCATATAAGACAATAATTAATCTTGGCACAGGGTAGGGAAAAAC 984
      |||

```

```

Sbjct 1141 AATTATGACCCGTGCCATATTAAGGCAAAATAATTAACCTTGGCACAGGGTAGGGAAAAAC 1200
Query 985 GTATATTGGCTCCAGGGGAAGGGAGTTGACCTGCAACTCAACAGTGACCAAGCATTAATT 1044
Sbjct 1201 ATATATTGGCTCCAGGGGAAGGGGTGTTTACCTGCAACTCAACAGTGACCAAGCATTAATT 1260
Query 1045 GCCAACATTGATACGGGAGATCAAAACAGATATTACCTTTAGTGACAGGTGGCAGAACTA 1104
Sbjct 1261 GCCAACATTGATACGGGAGATCAAAACAGATATTACCTTTAGTGACAGGTGGCAGAACTA 1320
Query 1105 TACCGATTGGAATTGGGAGATTACAAATTAGTAGAAATCACACCAATTGGCTTCGCACCT 1164
Sbjct 1321 TACCGATTGGAATTGGGAGATTACAAATTAGTAGAAATCACACCAATTGGCTTCGCACCT 1380
Query 1165 ACATCAGTAAAGAGATACTCCTCTGCTCACCAGAGACATACAAGA 1209
Sbjct 1381 ACATCAGTAAAGAGATACTCCTCTGCTCACCAGAGACATACAAGA 1425

```

Score = 579 bits (313), Expect = 1e-161  
 Identities = 323/328 (98%), Gaps = 0/328 (0%)  
 Strand=Plus/Plus

```

Query 1 ATGAAGGGTAGTAAGAATCAACTGCTGATTGCTATTGTACTAGCTAGTAGTGTACCTAACCA 60
Sbjct 1 ATGAAGGGTAGTAAGAATCAACTGCTGATTGCTATTGTACTAGCTAGTAGTGTACCTAACCA 60
Query 61 CATTGCAAGCAATTTGTGACTGTTTTCTATGGCATAACCCGCTGGAGGAATGCATCCATT 120
Sbjct 61 CATTGCAAGCAATTTGTGACTGTTTTCTATGGCATAACCCGCTGGAGGAATGCATCCATT 120
Query 121 CCCCTGTTTTGTGCAACCAAAAATAGAGATACTTGGGGAACCTGTACAGTGCTTGCACAGAC 180
Sbjct 121 CCCCTGTTTTGTGCAACCAAAAATAGAGATACTTGGGGAACCTGTACAGTGCTTGCACAGAC 180
Query 181 AATGATGATTATCAGGAAATAGCTTTAAATGTAACAGAGGCTTTCGATGATGGGATAAT 240
Sbjct 181 AATGATGATTATCAGGAAATAGCTTAAATGTAACAGAGGCTTTCGATGATGGGATAAT 240
Query 241 ACAGTAACAGAAACAAGCAGTGGAGGATGTCTGGAATCTATTGAGACATCAATAAAACCA 300
Sbjct 241 ACAGTAACAGAAACAAGCAGTGGAGGATGTCTGGAATCTATTGAGACATCAATAAAACCA 300
Query 301 TGTGTCAAATTAACACCCCTTATGTGTAG 328
Sbjct 301 TGTGTCAAATTAACACCCCTTATGTGTAG 328

```

Score = 536 bits (290), Expect = 8e-149  
 Identities = 310/319 (97%), Gaps = 3/319 (0%)  
 Strand=Plus/Plus

```

Query 336 CCATTGCAATACATCAGTCATCA--AAGAGTCATGTGATAAGCACTATTGGGATGCTATGA 394
Sbjct 582 CCATTGCAATACATCAGTCATCA--AGTCATGTGATAAGCACTATTGGGATGCTATGA 640
Query 395 GGTTTAGATACTGTGCACCACCGGGTTTTGCCCTACTAAGATGCAATGATATTAATTATT 454
Sbjct 641 GGTTTAGATACTGTGCACCACCGGGTTTTGCCCTACTAAGATGCAATGATATTAATTATT 700
Query 455 CAGGCTTTGCACCTAAATTGCTCTAAAGTAGTAGCTGCTACATGCACCAAGATGATGGAAA 514
Sbjct 701 CAGGCTTTGCACCTAAATTGCTCTAAAGTAGTAGCTGCTACATGCACCAAGATGATGGAAA 760
Query 515 CGCAATCTTCTACATGGTTTGGCTTTAATGGCACTAGAAACAGAAAATAGAACATATATCT 574
Sbjct 761 CGCAATCTTCTACATGGTTTGGATTTAATGGCACTAGAAACAGAAAATAGAACATATATAT 820
Query 575 ATTGGCATGGTAAAAATAACAGAAGTATTATCAGCTTAAATAACCTTTTATAATCTCACTA 634
Sbjct 821 ATTGGCATGGTAAAGATAACAGAAGTATTATCAGCTTAAATAACCTTTTATAATCTCACTA 880
Query 635 TGCATTGTAAGAG-GCCGG 652
Sbjct 881 TGCATTGTAAGGGTCCCG 899

```

>gb|J03654.1|HIV2NIHZ Human immunodeficiency virus type 2, isolate HIV2FG  
Length=9431

Sort alignments for this  
E value Score Percen  
Query start position

Score = 893 bits (483), Expect = 0.0  
Identities = 522/541 (96%), Gaps = 2/541 (0%)  
Strand=Plus/Plus

Query	670	AAACCCAGGCAAGCATGGTGTGGTTCAAAGGCCAATGGAAGGAAGCCATGCAGGAGGTG	729
Sbjct	7105	AAACCCAGGCAAGCATGGTGTGGTTCAAAGGCCAATGGAAGGAAGCCATGCAGGAGGTG	7164
Query	730	AAGGAGACCCCTTGCAGAACATCCAGATATAAAGGGAACAGGAGCCGCACAGAGAATATT	789
Sbjct	7165	AAGGAGACCCCTTGCAGAACATCCAGATATAAAGGGAACAGGAGCCGCACAGAGAATATT	7224
Query	790	AAATTTAAAGCACCAGGAAGAGGCTCAGACCCAGAAAGCAGATACATGTGGAATAACTGC	849
Sbjct	7225	AAATTTAAAGCACCAGGAAGAGGCTCAGACCCAGAAAGTAAACATACATGTGGAATAACTGC	7284
Query	850	AGAGGGGAATTTCTCTACTGCGACATGACTTGGTTCCTCAATTGGGTAGATAACAGGACG	909
Sbjct	7285	AGAGGAGAATCTCTCTACTGCAACATGACTTGGTTCCTCAATTGGGTAGAGAACAGGACG	7344
Query	910	GGTCAGAAACAGCGCAATTATGCACCGTGCATATAAGACAAATAATTAACTTTGGCAC	969
Sbjct	7345	GGTCAGAAACAGCGCAATTATGCACCGTGCCTATTAAGGCAATAATTAACTTTGGCAC	7404
Query	970	AGGGTAGGGAAAAA-CGTATATTTGCCTCCAGGGAAGGGGAGTTGACCTGCAACTCAAC	1028
Sbjct	7405	AGGGTAGGGAAAAATC-TATATTTGCCTCCAGGGAAGGGGAGTTGACCTGCAACTCAAC	7463
Query	1029	AGTGACCAGCATAATTGCCAACATTGATACGGGAGATCAAAACAGATATTACCTTTAGTGC	1088
Sbjct	7464	GGTGACCAGCATAATTGCCAACATTGATGCGGGAGATCAAAACAAATATTACCTTTAGTGC	7523
Query	1089	AGAGGTGGCAGAACTATACCGATTGGAATTGGGAGATTACAAATTAGTAGAAATCACACC	1148
Sbjct	7524	AGAGGCGGCAGAACTATACCGATTGGAATTGGGGGATTACAAATTAGTAGAAATCACACC	7583
Query	1149	AATTGGCTTCGCACCTACATCAGTAAAGAGATACTCCTCTGCTCACCAGAGACATACAAG	1208
Sbjct	7584	AATTGGCTTCGCACCTACATCAGTAAAGAGATACTCCTCTGCTCACCAGAGACATACAAG	7643
Query	1209	A 1209	
Sbjct	7644	A 7644	

Score = 551 bits (298), Expect = 3e-153  
Identities = 318/328 (96%), Gaps = 0/328 (0%)  
Strand=Plus/Plus

Query	1	ATGAAGGGTAGTAAAGAACTCACTGCTGATTGCTATTGTACTAGCTAGTGCTTACCTAACCA	60
Sbjct	6139	ATGAAGGGTAGTAAAGAACTCACTGCTGATTGCTATTGTACTAGCTAGTGCTTACCTAACCA	6198
Query	61	CATTGCAAGCAATTTGTGACTGTTTTCTATGGCATACCCGGTGGAGGAATGCATCCATT	120
Sbjct	6199	CATTGCAAGCAATTTGTGACTGTTTTCTATGGCATACCCGGTGGAGGAATGCATCCATT	6258
Query	121	CCCTGTTTTGTGCAACCAAAATAGAGATACTTGGGGAAGTGTACAGTGCTTGCAGAC	180
Sbjct	6259	CCCTGTTTTGTGCAACCAAAATAGAGATACTTGGGGAACAAATACAGTGCTTGCAGAC	6318
Query	181	AATGATGATTATCAGGAAATAGCTTTAAATGTAACAGAGGCTTTCGATGCATGGGATAAT	240
Sbjct	6319	AATGATGATTATCAGGAAATAACTCTAAATGTGACAGAGGCTTTCGATGCATGGGATAAT	6378
Query	241	ACAGTAACAGAACAAGCAGTGGAGGATGTCTGGAATCTATTGTAGACATCAATAAAACCA	300
Sbjct	6379	ACAGTAACAGAACAAGCAGTGGAGGATGTCTGGAATCTATTGTAGACATCAATAAAACCA	6438

Query 301 TGTGTCAAATTAACACCCCTTATGTGTAG 328  
 |||  
 Sbjct 6439 TGTGTCAAATTAACACCCCTTATGTGTAG 6466

Score = 551 bits (298), Expect = 3e-153  
 Identities = 316/325 (97%), Gaps = 0/325 (0%)  
 Strand=Plus/Plus

Query 336 CCATTGCAATACATCAGTCATCAAAGAGTCATGTGATAAGCACTATTGGGATGCTATGAG 395  
 |||  
 Sbjct 6717 CCATTGCAACACATCAGTCATCACAGAGTCATGTGATAAGCACTATTGGGATGCTATGAG 6776

Query 396 GTTTAGATACTGTGCACCACCGGGTTTGGCCCTACTAAGATGCAATGATATTAATTATTC 455  
 |||  
 Sbjct 6777 GTTTAGATACTGTGCACCACCGGGTTTGGCCCTACTAAGATGCAATGATATTAATTATTC 6836

Query 456 AGGCTTTGCACCTAATTGCTCTAAAGTAGTAGCTGCTACATGCACCAAGAATGATGGAAC 515  
 |||  
 Sbjct 6837 AGGCTTTGCACCTAATTGCTCTAAAGTAGTAGCTGCTACATGCACCAAGAATGATGGAAC 6896

Query 516 GCAATCTTCTACATGGTTTGGCTTTAATGGCACTAGAACAGAAAAAGAACATATATCTA 575  
 |||  
 Sbjct 6897 GCAATCTTCTACATGGTTTGGCTTTAATGGCACTAGAACAGAAAAAGAACATATATCTA 6956

Query 576 TTGGCATGGTAAAAATAACAGAACTATTATCAGCTTAAATAACTTTTATAATCTCAGTAT 635  
 |||  
 Sbjct 6957 TTGGCATGGTAAAGATAACAGAACTATTATCAGCTTAAATAACTTTTATAATCTCAGTAT 7016

Query 636 GCATTGTAAGAGCCGGGAAATAAG 660  
 |||  
 Sbjct 7017 GCATTGTAAGAGCCGGGAAATAAG 7041

>gb|U05355.1|HIV2U05355 Human immunodeficiency virus type 2 isolate HIV2CAM3, Gu  
 Bissau gp160 envelope (env) gene, complete cds  
 Length=2583

Sort alignments for this  
 E value Score Perce  
 Query start position

Score = 632 bits (342), Expect = 1e-177  
 Identities = 487/554 (87%), Gaps = 22/554 (3%)  
 Strand=Plus/Plus

Query 669 CAA-ACCAGGCCAAGCATGGTGTGGTTCAAAGGCCAATGGAAGGAAGCCATGCAGGAGG 727  
 |||  
 Sbjct 995 CAAGACCTAGGCCAAGCATGGTGTGGTTCAAAGGCCAATGGAAGGAAGCCATGCAGGAGG 1054

Query 728 TGAAGGAGACCCCTTGCAGAAACATCCAGATATAAAGGGAA-C-AGGAGCCGCACAGAGAA 785  
 |||  
 Sbjct 1055 TAAAGGAAACCCCTTGCAGAAACATCCAGGTATAAA-GGAACCAATGA---CACAAAGAA 1109

Query 786 TATTAAATTTAAAGCACCAGGAAGAGGCTCAGACCCAGAAGCAGCATACATGTGGACTAA 845  
 |||  
 Sbjct 1110 GATTAACTTTGCAGCACCAGGAAGAGGCTCAGACCCAGAGGTGACATACATGTGGACTAA 1169

Query 846 CTGCAGAGGGGAATTTCTCTACTGCGACATGACTTGGTTCCTCAATTTGGGTAGATAACAG 905  
 |||  
 Sbjct 1170 CTGCAGAGGGGAATTTCTCTACTGCAACATGACTTGGTTCCTCAATTTGGGTAGAGAACAG 1229

Query 906 GAC-G-G-GTCA-GAAACAGCGCAATTAATGCACCGTGCCATATAAGACAAATAATTAATA 961  
 |||  
 Sbjct 1230 AACTGAGAAT-AGGACATGGCACAATTATGTGCATGCCATATAAGGCAAAATAATTAACA 1288

Query 962 CTTGGCAGACGGGTAGGGAAAAAC-GTATATTTGCCTCCACGGGAAGGGGAGTTGACCTGC 1020  
 |||  
 Sbjct 1289 CCTGGCATAAAGTA-GGAAAAATGTATATTTGCCTCCACGGGAAGGGGAGTTAACCTGC 1347

Query 1021 AACTCAACAGTGACCAGCATAATTGCCAACATTGATACG-GGA-G-A--TCAACAGATA 1075  
 |||  
 Sbjct 1348 AACTCAACAGTGACCAGCATAATTGCTAATCATTTGA--CGTGGAGGCAATTCAGACAAATA 1405

Query 1076 TTACCTTTAGTGCAGAGGTGGCAGAACTATACCGATTGGAATTGGGAGATTACAAATTAG 1135



```

Sbjct 1406 TTACCTTTAGTGCAGAGGTGGCAGAACTATACCGATTGGAGTTGGGAGATTATAAATTGG 1465
Query 1136 TAGAAATCACACCAATTGGCTTCGCACCTACATCAGTAAAGAGATACTCCTCTGCTCACC 1195
Sbjct 1466 TAGAAATAACACCAATTGGCTTCGCACCTACATCAGAAAAGCGATACTCCTCTGCTCACA 1525
Query 1196 AGAGACATACAAGA 1209
Sbjct 1526 AGAGACATACAAGA 1539

```

Score = 438 bits (237), Expect = 2e-119  
 Identities = 297/326 (91%), Gaps = 4/326 (1%)  
 Strand=Plus/Plus

```

Query 336 CCATTGCAATACATCAGTCATCAAGAGTCATGTGATAAGCACTATTGGGATGCTATGAG 395
Sbjct 612 CCATTGCAACACATCAGTCATCAGAAATCATGTGATAAGCACTATTGGGATGCTATAAG 671
Query 396 GTTTAGATACTGTGCACCACCGGGTTTGGCCCTACTAAGATGCAATGATATTAATTATTC 455
Sbjct 672 GTTTAGATACTGTGCACCACCGGGTTATGCCCTGCTAAGGTGCAATGATACCAATTATTC 731
Query 456 AGGCTTTTGCA-CCTAATTGCTCTAAAGTAGTAGCTGTACATGCACCAAGATGATGGAAA 514
Sbjct 732 AGGCTTTG-AGGCCAATTGCTCTAAAGTAGTAGCTACTACATGCACCAAGATGATGGAAA 790
Query 515 CGCAATCTTCTACATGGTTTGGCTTTAATGGCACTAGAACAGAAAAATAGAACATATATCT 574
Sbjct 791 CACAAACTTCTACATGGTTTGGCTTTAATGGCAAGAGCAGAGAAATAGAACATATATCT 850
Query 575 ATTGGCATGGTAAAAATAACAGAACTATTATCAGCTTAAATAACTTTTATAATCTCAC-T 633
Sbjct 851 ATTGGCATGGTAGAGATAACAGAACTATCATCAGCTTAAACAAATATTATAATCTCTCTCT 910
Query 634 ATGCATTGTAAGAGGCCGGGAAATAA 659
Sbjct 911 -TGCAATTGTAAGAGGCCAGGAAATAA 935

```

Score = 405 bits (219), Expect = 2e-109  
 Identities = 285/317 (89%), Gaps = 3/317 (0%)  
 Strand=Plus/Plus

```

Query 15 GAATCAACTGCTGATTGCTATTGTACTAGTAGTGCCTTACCTAACACATTGCAAGC-A-A 72
Sbjct 15 GAATCAGCTGCTTTATTGCTATTTTACTAGTAGTGCCTTACTTAATATATTGCAGGCAACA 74
Query 73 -TTTGTGACTGTTTTCTATGGCATAACCGCGTGGAGGAATGCATCCATCCCTGTTTTG 131
Sbjct 75 GTATGTAACTGTTTTTATGGCATAACCGCGTGGAGGAATGCAACCATCCCTCTTTTG 134
Query 132 TGCAACCAAAAAATAGAGATACTTGGGGAAGTGTACAGTGCTTGCCAGACAATGATGATTA 191
Sbjct 135 TGCAACCAAAAAATAGAGATACTTGGGGAACCATACAGTGCTTGCCAGACAATGATGATTA 194
Query 192 TCAGGAAATAGCTTTAAATGTAACAGAGGCTTTTCGATGCATGGGATAATACAGTAACAGA 251
Sbjct 195 TCAGGAAATATCCTTGAATGTGACAGAGGCTTTTTCGATGCATGGGATAATACAGTAACAGA 254
Query 252 ACAAGCAGTGGAGGATGTCTGGAATCTATTGTAGACATCAATAAAACCATGTGTCAAAAT 311
Sbjct 255 ACAAGCAATAGAAGATGTCTGGAGTCTATTTCGAGACATCAATAAAGCCATGTGTCAAGTT 314
Query 312 AACACCCCTTATGTGTAG 328
Sbjct 315 AACACCCCTTATGTGTAG 331

```

>gb|U05351.1|HIV2U05351 Human immunodeficiency virus type 2 isolate HIV2CBL22 gp (env) gene, complete cds  
 Length=2556

Sort alignments for this  
 E value Score Percen

Query start position

Score = 617 bits (334), Expect = 3e-173  
 Identities = 469/532 (88%), Gaps = 18/532 (3%)  
 Strand=Plus/Plus

Query	670	AAACCCAGGCAAGCATGGTGTGGTTCAAAGGCGA-ATGGAAGGAAGCCATGCAGGAGGT	728
Sbjct	985	AAACCCAGAGCAAGCATGGTGTGGTTCCAAGGC-AGATGGAAGGAAGCCATGCAGGAGGT	1043
Query	729	GAAGGAGACCCCTTGCAGAAACATCCAGATATAAAGGGAA-CAGGAGCCGCACAGAGAATA	787
Sbjct	1044	GAAGCAAAACCTTGCAGAAACATCCAGGTATAAA-GGAACCA--A-CAATACAGAGAGTA	1099
Query	788	TTAAATTTAAAGCACCAGGAAGAGGCTCAGACCCAGAAGCAG-CATACATGTGGACTAAC	846
Sbjct	1100	TTACCTTTTACAGCACCAGGAGAGGCTCTGACCCAGAAG-TGACATACATGTGGACTAAC	1158
Query	847	TGCAGAGGGGAATTTCTCTACTGCACATGACTTGGTTCCTCAATTGGGTAGATAACAGG	906
Sbjct	1159	TGCAGAGGAGAATTCCTCTATTGCAACATGACTTGGTTCCTCAATTGGGTAGAAAAAATAG	1218
Query	907	ACGGGTGAGAAACAGCGCAATTATGCACCGTGCATATAA-GACAAATAATTAATACCTTG	965
Sbjct	1219	ACGGGTGAGACACAGCGCAACTATGTGCCGTGCATATAAAG-CAAATAATTAATACCTG	1277
Query	966	GCACAGGGTAGGGAAAAACGTATATTTGCCTCCAGGGAAGGGAGTTGACCTGCAACTC	1025
Sbjct	1278	GCATAAGGTAGGGAAAAATGTATATTTGCCTCCTAGGGAAGGGAGATTGCTCTGCAACTC	1337
Query	1026	AACAGTGACCAGCATTAATTGCCAACATTGAT--ACG-GG-AGATCAAAACAGATATTACCT	1081
Sbjct	1338	AACAGTGACCAGCATATCGCTAACATTGATGTAATGGTA-ATCAAAACAAATATTACCT	1396
Query	1082	TTAGTGCAGAGGTGGCAGAACTATACCGATTGGAATTGGGAGATTACAAATTAGTAGAAA	1141
Sbjct	1397	TTAGTGCAGAGGTGGCAGAACTATACCGATTGGAATTGGGAGATTATAAATTAGTAGAAA	1456
Query	1142	TCACACCAATTGGCTTCGCACCTACATCAGT-AAAGAGATACTCCTCTGCTC	1192
Sbjct	1457	TAACACCAATTGGCTTCGCACCTACAAACAGAGAAA-AGATACTCCTCTACTC	1507

Score = 416 bits (225), Expect = 1e-112  
 Identities = 294/327 (89%), Gaps = 6/327 (1%)  
 Strand=Plus/Plus

Query	336	CCATTGCAATACATCAGTCATCAAAAGGTCATGTGATAAGCACTATTGGGATGCTATGAG	395
Sbjct	597	CCATTGCAACAGCTCAGTCATCAAAAGGTCATGTGACAAGCACTATTGGGATGCTATGAG	656
Query	396	GTTTAGATACCTGTGCCACCACCGGGTTTTTGCCCTACTAAGATGCAATGATATTAAATATTC	455
Sbjct	657	GTTTAGATACCTGTGCCACCACCGGGTTTTTGCCCTGCTAAGATGCAATGATACCAATATTC	716
Query	456	AGGCTTTGCA-CCTAATTGCTCTAAAGTAGTAGCTGCTACATGCACCAGAATGATGGAAA	514
Sbjct	717	AGGCTTTG-AGGCCAATTGCTCTAAAGTAGTAGCTTCTACATGCACAAAGATGATGGAAA	775
Query	515	CGCAATCTTCTACATGGTTTGGCTTTAATGGCAGTGAAGCAGAAAAATAGAACATATATCT	574
Sbjct	776	CGCAATCTTCTACTTGGTTTGGCTTTAATGGCAGTGAAGCAGAAAAATAGAACATATATGT	835
Query	575	ATTGGCATGGTAAAA-ATAACAGAACTATTATCAGCTTAAATAA-CTTTTATAATCTCAC	632
Sbjct	836	ATTGGCATGG-AAGGGCAATAGAACTATTATCAGCTTGAACAAACATT-ATAATCTCAC	893
Query	633	TATGCAATTGTAAGAGGCCGGGAAATAA	659
Sbjct	894	CATACATTGTAAGAGGCCAGGAAATAA	920

Score = 399 bits (216), Expect = 1e-107  
 Identities = 288/322 (89%), Gaps = 8/322 (2%)  
 Strand=Plus/Plus

```

Query 11  GTAAGAA-TCAACTGC-TGATTGCTATTGTACTAGCTAGTCTTACCTAACACATTGCAA 68
Sbjct 8    GTAA-AATTCAGCTGCTTG-TTGCCATTTTGCTAACTAGTCTTGCTTTAGTATATTGCAC 65
Query 69  GCAATTTGTGACTGTTTTCTATGGCA-TACCCGCGTGGAGGAATGCATCCATTCCCTGT 127
Sbjct 66  CCAATATGTGACTGTTTTCTATGG-AGTACCCGCGTGGAGGAATGCATCCATCCCCCTCT 124
Query 128  TTTGTGCAACCAAAAATAGAGATACTTGGGGAACGTACAGTGCTTGCCAGACAATGATG 187
Sbjct 125  TTTGTGCAACCAAAAATAGAGATACTTGGGGAACCATACAGTGCTTGCCAGACAATGATG 184
Query 188  ATTATCAGGAAATAGCTTTAAATGTAACAGAGGC-TTTCGATGCATGGGATAATACAGTA 246
Sbjct 185  ATTATCAAGAGCTAACTTTAAATGTAACAGAGGCCTTT-GATGCATGGGATAATACAGTA 243
Query 247  ACAGAAACAGCAGTGGAGGATGCTCGGAATCTATTGAGACATCAATAAAACCATGTGTC 306
Sbjct 244  ACAGAAACAGCAATAGAGATGCTCGGCATCTATTGAGACATCAATAAAACCATGTGTC 303
Query 307  AAATTAACACCCCTTATGTGTAG 328
Sbjct 304  AAATTAACACCTTTATGTGTAG 325

```

>gb|AF170050.1|AF170050 HIV-2 isolate 96325 from France envelope glycoprotein (e partial cds  
Length=1688

Sort alignments for this  
E value Score Percent  
Query start position

```

Score = 614 bits (332), Expect = 4e-172
Identities = 469/532 (88%), Gaps = 24/532 (4%)
Strand=Plus/Plus

Query 672  ACCCAGGCAAGCATGGTGTGGTTCAAAGCGCAATGGAAG-GAAGCCATGCAGGAGGTGA 730
Sbjct 293  ACCTAGGCAAGCATGGTGTGGTTCAAAGCGCAGTGG-AGAGAAGCCATGCAGGAGGTGA 351
Query 731  AGGAGACCCCTTGCGA-AACATCCCAGATATAAAGGGAA-CAGGAGCCGCACAGA-GAATA 787
Sbjct 352  AGGAGACCCCTTGCG-ARMCATCCCAGGTATAAA-AGAATCA--A-TGGCACA-AMCAATA 405
Query 788  TTAATTTT--AAAGCACCAGGAAGAGGCTCAGACCCAGAAGCAGCATACATGTGGACTAA 845
Sbjct 406  TTAATTTTGCAAA--ACCAGGAAGTGGCTCAGACCCAGAAGTGGCATACTGTGGACTAA 463
Query 846  CTGCAGAGGGGAATTTCTCTACTGCGACATGACTTGGTTCCTCAATTGGGTAGATAACAG 905
Sbjct 464  CTGCAGAGGAGAAATTTCTCTACTGCAACATGACTTGGTTCCTCAATTGGGTAGAGAACAG 523
Query 906  GACGGGTCAGAAACAGCGCAATTATGCACCGTGCCATATAA-GACAAATAATTAATACCT 964
Sbjct 524  TACGAATCAGACACAAACAAATATGCGCCGTGCCATATAAAG-CAATAATTAATACCT 582
Query 965  GGCACAGGGTAGGGAACGATATATTGCTCCCGAGGGAAGGGAGTGTGACCTGCAACT 1024
Sbjct 583  GGCACAGAGTAGGGAACGATATATTGCTCCCTAGGGAAGGAGAGTGTAACTGCAACT 642
Query 1025  CAACAGTGACACAGCATAATTGCCAACATTGA--TACGGGAGATCA--A-ACAGATATTAC 1079
Sbjct 643  CAACAGTGACACAGCATAATTGCTAACATTGACGTA-GGCA-ATAACRAGACAAATATTAC 700
Query 1080  CTTTAGTGACAGGTGGCAGAACTATACCGATTGGAATTTGGGAGATTACAAATAGTAGA 1139
Sbjct 701  CTTTAGTGACAGGTGGCAGAACTGTACCGATTGGAATTTGGGAGATTATAAATTAATAGA 760
Query 1140  AATCACACCAATTGGCTTCGCACCTACATCAGTAAAGAGATACCTCTCTGCT 1191
Sbjct 761  AGTGACACCAATTGGCTTCGCACCTACATCAGAAAAAGATACCTCTCTGCT 812

```

Score = 270 bits (146), Expect = 9e-69  
Identities = 204/232 (87%), Gaps = 4/232 (1%)

Strand=Plus/Plus

Query	431	TAAGATGCAATGATATTAATTATTTCAGGCTTTGCA-CCTAATTGCTCTAAAGTAGTAGCT	489
Sbjct	1	TAAGATGCAATGATACCAATTATTTCAGGCTTTG-AGCCCAATTGTTCTAAAGTAGTAGCT	59
Query	490	GCTACATGCAACAGAAATGATGGAAACGCAATCTTCTACATGGTTTGGCTTTAATGGCACT	549
Sbjct	60	GCTACATGCAACAGAAATGATGGAGACGCAACCTCCACTTGGTTTGGCTTTAATGGCACT	119
Query	550	AGAACAGAAAAATAGAACATATATCTATTGGCATGGTAAAAATAACAGAACTATTATCAGC	609
Sbjct	120	AGGGCAGTAAATAGAACATTTATCTATTGGCATGGCAGGGATAATAGGACTATTATCAGC	179
Query	610	TTAAATAA-CTTTTATAATCTCACTATGCATTGTAAGAGGCCGGGAAATAAG	660
Sbjct	180	TTAAACAAGC-ATTATAATCTCACTATGCATTGTAAGAGGCCAGGAAACAAG	230

>gb|AF170042.1|AF170042 HIV-2 isolate 96308 from France envelope glycoprotein (e partial cds  
Length=1779

Sort alignments for this  
E value Score Percen  
Query start position

Score = 612 bits (331), Expect = 1e-171  
Identities = 476/544 (87%), Gaps = 18/544 (3%)  
Strand=Plus/Plus

Query	678	GCAAGCATGGTGTGGTTTCAAGGCGAATGGAAGGAAGCCATGCAGGAGGTGAAGGAGAC	737
Sbjct	346	GCAAGCATGGTGTGGTTTCAAGGCGAATGGAAGGAAGCCATGCAGGAGGTGAAGGAGAC	405
Query	738	CCTTGGCAAAACATCCCAGATATAAAGGGAA-CAGGAGCCGCACAGAGAATATTAAATTTA	796
Sbjct	406	CCTTGGCAAAACATCCCAGGTACAAA-GGAACCA--A-TAAACCGAGAATATTACCTTTA	461
Query	797	AAGCACCAGGAAGAGGCTCAGACCAGCAAGCAGCATACATGTGGACTAAGTGCAGAGGGG	856
Sbjct	462	CAGCACCAGGAAAAGGCTCAGACCAGCAAGTAGCATACATGTGGACTAAGTGCAGAGGAG	521
Query	857	AATTTCTCTACTGCGACATGACTTGGTTCCCTCAATTGGGTAGATAACAG---GAC-GG--	910
Sbjct	522	AATTTTGTACTGCAACATGACTTGGTTCCCTCAATTGGATAGAAAACAGAACTACTGGAA	581
Query	911	GTGAGAAACAGCGCAATTATGCAACCGTGCCATAT-AAGACAAATAATTAACTTTGGCAC	969
Sbjct	582	ATCATACATGGGCACAAATTATGTAACCGTGCCATATAAG-CAAAATTATTAATACCTTGCAT	640
Query	970	AGGGTAGGGAAAAACGTATATTGGCTCCCAGGGAAGGGGAGTTGACCTGCAACTCAACA	1029
Sbjct	641	AAAGTAGGGAAAAATGTATATTGGCTCCCAGGGAAGGGGAATTAACCTGCAACTCAACA	700
Query	1030	GTGACCAGCATAAATGCCAACATTGATAC-GG-GAG-ATCAACAGATATTACCTTTAGT	1086
Sbjct	701	GTGAGCAGCATAAATGCCAACATTGATACAGGTGGGAATCAACCAATATTACCTTTAGT	760
Query	1087	GCAGAGGTGGCAGAACTATACCGATTGGAATTGGGAGATTACAAATTAGTAGAAATCACA	1146
Sbjct	761	GCAGAGGTGGCAGAACTGTACCGATTGGAATTGGGAGATTATAAATTAGTAGAAATAACA	820
Query	1147	CCAATTGGCTTCGCACCTACATCA-GTAAAGAGATACTCCTCTGCTCACCAGAGACATAC	1205
Sbjct	821	CCAATTGGCTTCGCACCTACAG-ATGTAAAGAGATACTCCTCTACTCATGAGAGACATAA	879
Query	1206	AAGA 1209	
Sbjct	880	AAGA 883	

Score = 379 bits (205), Expect = 1e-101  
Identities = 255/279 (91%), Gaps = 3/279 (1%)  
Strand=Plus/Plus

```

Query 383 GGGATGCTATGAGGTTTAGATACTGTGCACCACCGGGTTTTGCCCTACTAAGATGCAATG 442
          |||||
Sbjct 1 GGGATG-TATGAGGTTTAGATACTGTGCACCACCGGGTTTTGCCCTGCTAAGATGCAATG 59

Query 443 ATATTAATTATTCAGGCTTTGCACCTAATTGCTCTAAAGTAGTAGCTGTACATGCACCA 502
          |||||
Sbjct 60 ATACCAATTATTCAGGCTTTGAACCAATTGCTCTAAAGTAGTAGCTACCACTTGCACTA 119

Query 503 GAATGATGGAACCGCAATCTTCTACATGGTTTGGCTTTAATGGCACTAGAACAGAAAAATA 562
          |||||
Sbjct 120 GAATGATGGAACCGCAATCTTCTACATGGTTTGGCTTTAATGGCACTAGAGCAGAAAAATA 179

Query 563 GAACATATATCTATTGGCATGGTAAAA-ATAACAGAACTATTATCAGCTTAAATAACTTT 621
          |||||
Sbjct 180 GGACATATATCTATTGGCATGG-AAGGGATAACAGAACTATCATCAGCTTGAATAAAATTT 238

Query 622 TATAATCTCACTATGCATTGTAAGAGGCCGGGAAATAAG 660
          |||||
Sbjct 239 TATAATCTCAGTGTGTATTGTAAGAGGCCAGGAAATAAG 277

```

>gb|U05352.1|HIV2U05352 Human immunodeficiency virus type 2 isolate HIV2CBL23 gp (env) gene, complete cds  
Length=2580

Sort alignments for this  
E value Score Percen  
Query start position

```

Score = 599 bits (324), Expect = 1e-167
Identities = 464/528 (87%), Gaps = 23/528 (4%)
Strand=Plus/Plus

Query 672 ACCCAGGCAGCATGGTGTGGTTCAAAGGCGAATGGAAGGAAGCCATGCAGGAGGTGAA 731
          |||||
Sbjct 987 ACCCAGACAGCATGGTGTGGTTCAAAGGTGAATGGAAGGGAGCCATGCAGGAGGTGAA 1046

Query 732 GGAGACCCCTTGCAGAAACATCCCAGATATAAAGGGAA-C-AGGAGCCGCACAGAGAATATT 789
          |||||
Sbjct 1047 GGAAACCCCTTGCAGAAACATCCCAGGTATAAA-GGAACCAATGA----AACAAAGAAATATT 1101

Query 790 AAATTTAAAGCACCAGG-AAGAGGCTCAGACCCAGAAAGCAGCATACTGTGGACTAACTG 848
          |||||
Sbjct 1102 AACTTTACAGCACCAGGAAGG-GGCTCAGACCCAGAGGTGGCATACTGTGGACTAACTG 1160

Query 849 CAGAGGGGAATTTCTCTACTGCGACATGACTTGGTTCCCTCAATTGGGTAGATAACAGGAC 908
          |||||
Sbjct 1161 CAGAGGAGAATTTCTCTACTGCAACATGACTTGGTTCCCTCAATTGGGATAG--AA-A--A- 1214

Query 909 GGGTCAGAAACAGCGCAATTATGCACCGTGCCATATAAGACAAAATAATTAATACCTGGCA 968
          |||||
Sbjct 1215 ---TAAGACACACCGCAATTATGTACCGTGCCATATAAGACAAAATAATTAACACCTGGCA 1271

Query 969 CAGGGTAGGGAACGTAATTTGCCTCCAGGGAAGGGGAGTTGACCTGCAACTCAAC 1028
          |||||
Sbjct 1272 TAAGGTAGGGAACGTAATTTGCCTCCAGGGAAGGGGAGTTGACCTGCAACTCAAC 1331

Query 1029 AGTGACCAGCATAATTGCCAACATTGATACG---GGAGATCAA-ACAGATATTACCTTTA 1084
          |||||
Sbjct 1332 AGTAACTAGCATAATTGCTAACATTGATGCAAAATGGAAAT-AATACAGATATTACCTTTA 1390

Query 1085 GTGCAGAGGTGGCAGAACTATACCGATTGGAATTTGGGAGATTACAAATTAGTAGAAATCA 1144
          |||||
Sbjct 1391 GTGCAGAGGTGGCAGAACTATACCGATTAGAGTTGGGAGATTATAAATTTGGTAGAAATAA 1450

Query 1145 CACCAATTGGCTTCGCACCTACATCAGTAAAGAGATACCTCTCTGCTC 1192
          |||||
Sbjct 1451 CACCAATTGGCTTCGCACCTACAGCAGAAAAAGATACCTCTCTACTC 1498

```

Score = 479 bits (259), Expect = 1e-131  
Identities = 303/325 (93%), Gaps = 0/325 (0%)  
Strand=Plus/Plus

```

Query 336 CCATTGCAATACATCAGTCATCAAGAGTCATGTGATAAGCACTATTGGGATGCTATGAG 395
          |||||

```

```

Sbjct 597 CCATTGCAACACATCGGTCATCACAGAGTCATGTGACAAAGCACTATTGGGATGCTATGAG 656
Query 396 GTTTAGATACTGTGCACCACCGGGTTTGGCCCTACTAAGATGCAATGATATTAATTATTC 455
Sbjct 657 GTTTAAATACTGTGCACCACCGGGTTTGGCCCTACTAAGATGCAATGATACCAATTATTC 716
Query 456 AGGCTTTGCACTTAATTGCTCTAAAGTAGTAGCTGCTACATGCACCAGAATGATGGAAAC 515
Sbjct 717 AGGCTTTGCGCCCAATTGCTCTAAGTAGTAGCTGCTACATGCACCAGAATGATGGAAAC 776
Query 516 GCAATCTTCTACATGGTTTGGCTTTAATGGCACTAGAACAGAAAATAGAACATATATCTA 575
Sbjct 777 GCAAACTTCTACATGGTTTGGCTTTAATGGCACTAGAGCAGAAAATAGAACATTATCTA 836
Query 576 TTGGCATGGTAAAAATAACAGAACTATTATCAGCTTAAATAACTTTTATAATCTCACTAT 635
Sbjct 837 TTGGCATGGTAGGATAACAGAACTATCATCAGCTTAAACAAATATTATAATCTCACTAT 896
Query 636 GCATTGTAAGAGGCCGGGAAATAAG 660
Sbjct 897 ACATTGTAAGAGGCCAGGAAATAAG 921

```

Score = 418 bits (226), Expect = 3e-113  
 Identities = 297/331 (89%), Gaps = 6/331 (1%)  
 Strand=Plus/Plus

```

Query 1 ATGAAGGGTAGTAAG-AATCAACTGC-TGATTGCTATTGTACTAGCTAGTGCTTACCTAA 58
Sbjct 1 ATGATGGGTGGT-AGAAATCAGCTGCTTG-TTGCCTATTTGCTAGCTAGTACTGTCTGA 58
Query 59 CACATTGCAAGCAATT-TGTGACTGTTTTCTATGGCATACCCGCGTGGAGGAATGCATCC 117
Sbjct 59 TATATTGC-ACCAATTATGTGACTGTTTTCTATGGCATACCCGCGTGGAGGAATGCATCC 117
Query 118 ATTCCCTCTTTTGTGCAACCAAAATAGAGATACTTTGGGGAACGTACAGTGCTTGCCA 177
Sbjct 118 ATTCCCTCTTTTGTGCAACCAAGGAATAGGGATACCTTTGGGGAACCATACAGTGCTTGCCA 177
Query 178 GACAAATGATGATTATCAGGAAATAGCTTTAAATGTAACAGAGGCTTTCGATGCATGGGAT 237
Sbjct 178 GACAAATGATGATTATCAGGAGATAAAGTTGAATGTGACAGAGGCTTTCGATGCATGGGAT 237
Query 238 AATACAGTAACAGAAACAGCAGTGGAGGATGCTCGGAATCTATTIGAGACATCAATAAAA 297
Sbjct 238 AATACAGTAACAGAAACAGCAATAGAGATGCTCGGAATCTATTIGAGACATCAATAAAA 297
Query 298 CCAATGTGTCAAATTAACACCCCTTATGTGTAG 328
Sbjct 298 CCAATGTGTCAAATTAACGCCCTTATGTGTAG 328

```

>gb|DQ213030.1| HIV-2 isolate P2-1996 from Sweden envelope glycoprotein (env)  
 gene, partial cds  
 Length=1575

Sort alignments for this  
 E value Score Percen  
 Query start position

Score = 597 bits (323), Expect = 4e-167  
 Identities = 467/533 (87%), Gaps = 24/533 (4%)  
 Strand=Plus/Plus

```

Query 672 ACCCAGGCAAGCATGGTGTGGTTCAAAGGCGAA-TGGAAGGAAGCCATGCAGGAGGTGA 730
Sbjct 1038 ACCCAGGCAAGCATGGTGTGGTTCAAAGGC-AAGTGGAGGGAAGCCATGCAGGAGGTAA 1096
Query 731 AGGAGACCCCTTGCAGAAA-CATCCCAGATATAAAGGGAA-CAGGAGCCGCACA-G-AGAAT 786
Sbjct 1097 AGCAAAACCCCTTGC-AAACCATACCAGATATAAA-GGAACCA--A---ATACATGAAGAAT 1149
Query 787 ATTAAATTTTAAAGCACCAGGAAGAGGCTCAGACCCAGAGCAGCATACATGTGGACTAAC 846
Sbjct 1150 ATTACCTTTTGAAGCACCAGGAAGAGGCTCAGACCCAGAGAGTGGCATACATGTGGACTAAT 1209

```

```

Query 847   TGCAGAGGGGAATTTCTCTACTGCGACATGACITGGTTCCCTCAATTGGGTAGATAACAGG 906
          |||
Sbjct 1210   TGCAGAGGAGAATTTCTCTACTGCAACATGACITGGTTCCCTCAATTGGGTAGAAAAACAA 1269
          |||
Query 907   ACGGGTCAGAAACAGCGCAATTATGCACCGTGCCATATAA-GACAAATAATTAATACTTG 965
          |||
Sbjct 1270   ACAAATCAGATACAGCGCAATTATGTGCCATGCCATATAAAG-CAATAATTAATACTTG 1328
          |||
Query 966   GCACAGGGTAGGGAAAAACGTATATTTCCTCCAGGGAAGGGAGTTGACCTGCAACTC 1025
          |||
Sbjct 1329   GCACAGGGTAGGGAAAAATGTATATTTCCTCCAGGGAAGGAGAGTTGCTCTGCAATTC 1388
          |||
Query 1026  AACAGTGACCAGCATAATTGCCAACATTGA--TAC--GGGAGATCAA-ACAGA-TATTAC 1079
          |||
Sbjct 1389   CTCAGTGACCAGCATAATCGCTAACATTGACATACTAGGGA-A-CAAGAC-GAATATTAC 1445
          |||
Query 1080  CTTTAGTGACAGGTGGCAGAACTATACCGATTGGAATTGGGAGATTACAAATTAGTAGA 1139
          |||
Sbjct 1446  CTTTAGTGACAGGTGGCAGAACTATACCGATTGGAATTGGGAGATTATAAATTAATAGA 1505
          |||
Query 1140  AATCACACCAATTGGCTTCGCACCTACATCAGTAAAGAGATACCTCTGCTC 1192
          |||
Sbjct 1506  AGTGACACCAATTGGCTTCGCACCTACATCAGAAAAGAGATACCTCTGCTC 1558
          |||

```

Score = 381 bits (206), Expect = 4e-102  
 Identities = 288/328 (87%), Gaps = 4/328 (1%)  
 Strand=Plus/Plus

```

Query 335   GCCATTGCAATACATCAGTCATCAAAGAGTCATGTGATAAGCACTATTGGGATGCTATGA 394
          |||
Sbjct 650   GCCATTGCAACACATCAGTCATCAGAGTCATGTGATAAGCACTATTGGGATGCTATGA 709
          |||
Query 395   GGGTTAGATACTGTGACCACCGGGTTTGGCCCTACTAAGATGCAATGATATTAATTATT 454
          |||
Sbjct 710   GATTAGATACTGTGACCACCGGGATACATCCTACTAAGATGTAATGATACCAATTATT 769
          |||
Query 455   CAGGCTTTGCACCTAATTGCTCTAAAGTAGTAGCTGCTACATGCACACAGA-ATGATGGAA 513
          |||
Sbjct 770   CAGGCTTTGAACTAATTGTTCTAAAGTAGTAGCTTCACATGCACAAGGGA-GATGGAG 828
          |||
Query 514   ACGCA-ATCTTCTACATGGTTTGGCTTTAATGGCACTAGAACAGAAAAATAGAACATATAT 572
          |||
Sbjct 829   ACGCAGACCTCC-ACCTGGTTTGGCTTTAATGGCACTAGAGCAGAAAAATAGAACATATAT 887
          |||
Query 573   CTATTGGCATGGTAAAAATAACAGAACTATTATCAGCTTAAATAACCTTTTATAATCTCAC 632
          |||
Sbjct 888   CTATTGGCATGGTAGAGATAATAGGACTATTATTAGCTTAAACAAGAGTTATAGTCTCAA 947
          |||
Query 633   TATGCATTGTAAGAGGCCGGGAAATAAG 660
          |||
Sbjct 948   GATACATTGTAAGAGGCCAGGAAACAAG 975
          |||

```

Score = 368 bits (199), Expect = 3e-98  
 Identities = 280/319 (87%), Gaps = 6/319 (1%)  
 Strand=Plus/Plus

```

Query 11   GTAAGAATCAACT-GCTGATTGCTA--TTGTACTAGCTAGTGCTTACCTAACACATTGCA 67
          |||
Sbjct 8     GTAGGAATCAACTAGTTG-TTGCCAGCTTG--CTAGCTATTGTTTGGCTTAGTATATTGCA 64
          |||
Query 68   AGCAATTGTGACTGTTTTCTATGGCATACCCGCGTGAGGAAATGCATCCATCCCTGT 127
          |||
Sbjct 65   CTCAGTATGTGACTGTTTTCTATGGCATACCCGCGTGAGGAAATGCATCCATCCCTCT 124
          |||
Query 128  TTTGTGCAACCAAAAAATAGAGATACTTGGGGAACGTACAGTGCTTGCCAGACAATGATG 187
          |||
Sbjct 125  TTTGTGCAACCAAAAAATAGAGACACCTGGGGAACCATACAGTGCTTACCAGACAATGATG 184
          |||
Query 188  ATTATCAGGAAATAGCTTTAAATGTAACAGAGGCTTTCGATGCATGGGATAATACAGTAA 247
          |||
Sbjct 185  ACTATCAGGAAATACCTTTAAATGTAACAGAGGCTTTCGACGCGTGGGATAATACAGTAA 244
          |||
Query 248  CAGAACAGCAGTGGAGAGATGTCTGGAATCTATTGTAGACATCAATAAAACCATGTGTCA 307
          |||

```

```

Sbjct 245 CAGAACAGGCAATAGAAGATGTCTGGAATCTATTTCGAGACATCAATAAAACCATGCGTCA 304
Query 308 AATTAACACCTTTATGTGT 326
      |||||
Sbjct 305 AATTAACACCTTTATGTGT 323

```

```

>gb|AF170047.1|AF170047 HIV-2 isolate 96330 from France envelope glycoprotein (e
partial cds
Length=1993

```

```

Sort alignments for this
E value Score Perce
Query start position

```

```

Score = 597 bits (323), Expect = 4e-167
Identities = 464/531 (87%), Gaps = 13/531 (2%)
Strand=Plus/Plus

```

```

Query 669 CAA-ACCCAGGCAAGCATGGTGTGGTTCAAAGGCGAA-TGGAAGGAAGCCATGCAGGAG 726
      |||
Sbjct 585 CAAGACCCAGGCAAGCATGGTGTGGTTCAAAGGCGAA-AAGTGAAGGAGGCCATGCAGGAG 643
      |||
Query 727 GTGAAGGAGACCCCTTGCAGAAACATCCAGATATAAAGGGAA-CAGGAGCCGCACAGAGAA 785
      |||
Sbjct 644 GTGAAGGAACCCCTTGCAGAAACATCCAGGTATACA-GGAACCA--A-CAAAACGGAGAA 699
      |||
Query 786 TATTAATTTTAAAGCACCAGGAAGAGGCTCAGACCCAGAAGCAGCATACATGTGGACTAA 845
      |||
Sbjct 700 TATTACITTTACAGCGCCAGGAAAAGGCTCAGACCCAGAGGTGGCATACATGTGGACTAA 759
      |||
Query 846 CTGCAGAGGGGAATTTCTCTACTGCGACATGACTTGGTTCCTCAATTGGGTAGATAACAG 905
      |||
Sbjct 760 CTGCAGAGGAGAATTTTCTCTACTGCAATATGACTTGGTTCCTCAATTGGGTAGAAAACAG 819
      |||
Query 906 GACGGGTGAGAAACAGCGCAATTATGACACCGTGCCATAT-AAGACAAATAATTAACTT 964
      |||
Sbjct 820 AACGAATCAGATACGGGACAAATTATGTGCCATGCCATATAAG-CAATAATTAATACCT 878
      |||
Query 965 GGCACAGGGTAGGGAAAAACGTATATTTGCTCTCCAGGGAAGGGGAGTTGACCTGCAACT 1024
      |||
Sbjct 879 GGCACAGGGTAGGGAAAAACGTATATTTGCTCTCAGGGAAGGAGAGTTGACCTGCAACT 938
      |||
Query 1025 CAACAGTGACCCAGCATATTTGCCAACATTGA--TAC-GGGAGATCAACAGATATTACCT 1081
      |||
Sbjct 939 CCACAGTGACCCAGCATATTTGCTAACATTGACGACACAAGAAAACAGCAAAATATTACCT 998
      |||
Query 1082 TTAGTGCAGAGGTGGCAGAACTATACCGATTGGAATTGGGAGATTACAAATAGTAGAGAA 1141
      |||
Sbjct 999 TTAGTGCAGAGGTGGCAGAACTATACCGATTAGAACTGGGAGATTACAAATTAATAGAGG 1058
      |||
Query 1142 TCACACCAATTGGCTTCGCACCTACATCAGTAAAGAGATACTCCTCTGCTC 1192
      |||
Sbjct 1059 TAACACCAATTGGCTTCGCACCTACATCAGAAAAAAGATACTCCTCTGCTC 1109
      |||

```

```

Score = 375 bits (203), Expect = 2e-100
Identities = 285/324 (88%), Gaps = 7/324 (2%)
Strand=Plus/Plus

```

```

Query 336 CCATTGCAATACATCAGTCATCAAAGAGTCATGIGATAAGCACTATTGGGATGCTATGAG 395
      |||
Sbjct 202 CCATTGCAACATACATCAGTCATCAGAGATCATGTGATAAGCACTATTGGGATGCTATGAG 261
      |||
Query 396 GTTTAGTACTGTGACCACCGGGTTTGGCCCTACTAAGATGCAATGATATTAATTATTC 455
      |||
Sbjct 262 GTTTAGTACTGTGACCACCGGGTTTGGCCCTACTAAGATGCAATGATACCAATATTC 321
      |||
Query 456 AGGCTTTTGA-CCTAATTGCTCTAAAGTAGTAGCTGTACATGCACCAGA-ATGATGGAA 513
      |||
Sbjct 322 AGGCTTTTGA-AGGCCAACTGTTCTAAAGTAGTAGCTTCTACATGTACAGAGAA-ATGGAA 379
      |||
Query 514 ACGCA-ATCTTCTACATGGTTTGGCTTTAATGGCACTAGAACAGAAAATAGAACATATAT 572
      |||
Sbjct 380 ACGCAGA-CTTCACATTGGTTTGGCTTTAATGGCACTAGGCGGAAAATAGAACATATAT 438
      |||

```



```

Query 573 CTATTGGCATGGTAAAAATAACAGAACTATTATCAGCTTAAATAACITTTATAATCTCAC 632
          |||
Sbjct 439 CTATTGGCATGGTAGAGACAATAGGACTATCATTAGCTTAAACAAGTATTATAATCTCAC 498

Query 633 TATGCATTGTAAGAGGCC--GGAA 655
          |||
Sbjct 499 CATACGTTGTAAGAGACCAGGGAA 522

```

```

>gb|U05350.1|HIV2U05350 Human immunodeficiency virus type 2 isolate HIV2CBL21 gp
(env) gene, complete cds
Length=2601

```

```

Sort alignments for this
E value Score Percent
Query start position

```

```

Score = 595 bits (322), Expect = 1e-166
Identities = 463/530 (87%), Gaps = 14/530 (2%)
Strand=Plus/Plus

```

```

Query 670 AAACCCAGGCAAGCATGGTGTGGTTCAAAGGCGAA--TGGAAGGAAGCCATGCAGGAGGT 728
          |||
Sbjct 997 AAACCCATGCAAGCATGGTGTGGTTCGAAGG--TAAGTGGAGGGAAGCCATGCAGGAGGT 1055

Query 729 GAAGGAGACCCCTTGCAGAAACATCCAGATATAAAGGGAA--CAGGAGCCGCACAGAGAATA 787
          |||
Sbjct 1056 GAAGCAGACCCCTTGTAAACATCCAGGTATAGA--GGAACCA--ATAAG--ACAGAAAATA 1111

Query 788 TTAAATTTAAAGCACCAGGAAGA--GGCTCAGACCCAGAAGCAGCATACATGTGGACTAAC 846
          |||
Sbjct 1112 TTACCTTTGCAGGACCAAGG--AGAGGGCTCAGACCCAGAAGTGGCATACATGTGGACTAAC 1170

Query 847 TGCAGAGGGGAATTTCTCTACTGCGACATGACTTGGTTCCTCAATTGGGTAGATAACAGG 906
          |||
Sbjct 1171 TGCAGAGGGAATTTCTCTACTGCAACATGACTTGGTTCCTCAATTGGGTGGAGAACACA 1230

Query 907 ACGGGTCAGAAACAGCGCAATTATGCAACCGTGCCATATAAGACAAATAATTAACTTGG 966
          |||
Sbjct 1231 ACAAAATCAGACACAAACAAATTATGTGCCATGCCATATAAGGCAAAATAATTAACTCTGG 1290

Query 967 CACAGGGTAGGGAAAAACGTATATTTCCTCCAGGGAAGGGGAGTTGACCTGCAACTCA 1026
          |||
Sbjct 1291 CACAAGGTAGGGAAAAATGTATATTTCCTCCAGGGAAGGACTGTTGTCTGCAACTCA 1350

Query 1027 ACAGTGACCAGCATAATTGCCAACATTGTATCG---GG--AGATCAACAGATATTACCTT 1082
          |||
Sbjct 1351 ACAGTGACCAGCATAATTGCTAACATTGTATACATACGGTA--ACCAGACAGATATTACCTT 1409

Query 1083 TAGTGCAGAGGTGGCAGAACTATACCGATTGGAATTTGGGAGATTACAAATTAGTAGAAAT 1142
          |||
Sbjct 1410 TAGTGCAGAGGTGGCAGAACTATACCGATTGGAACCTGGGAGATTATAAATTAGTAGAGAT 1469

Query 1143 CACACCAATTGGCTTCGCACCTACATCAGTAAAGAGATACTCCTCTGCTC 1192
          |||
Sbjct 1470 CACACCAATTGGCTTCGCACCTACATCAGTAAAGAGATACTCCTCTGCTC 1519

```

```

Score = 414 bits (224), Expect = 4e-112
Identities = 294/328 (89%), Gaps = 4/328 (1%)
Strand=Plus/Plus

```

```

Query 335 GCCATTGCAATACATCAGTCATCAAAGAGTCATGTGATAAGCACTATTGGGATGCTATGA 394
          |||
Sbjct 608 GCCATTGCAACATCAGTCATCAGAGTCATGTGATAAGCACTATTGGGATGCTATGA 667

Query 395 GGTTTAGATACTGTGCACACCGGGTTTGGCCCTACTAAGATGCAATGATATTAATTATT 454
          |||
Sbjct 668 GGTTTAGATACTGTGCACACCGGGTTTGGCCCTACTAAGATGCAATGATACCAATATT 727

Query 455 CAGGCTTTGCA--CCTAATTGCT--CTAAAGTAGTAGCTGCTACATGCACCAAGATGATGGA 512
          |||
Sbjct 728 CAGGCTTTG--AGCCCAATTG--TACTAAGTAGTAGCTTCTACATGCACCAAGGATGATGGA 785

Query 513 AACGCAATCTTCTACATGGTTTGGCTTTAATGGCACTAGAACAGAAAATAGACATATAT 572
          |||

```

```

Sbjct 786 AACGCAAACTCCACTTGGTTTGGCTTTAATGGCACTAGGGCAGAGAATAGAACATATAT 845
Query 573 CTATTGGCATGGTAAAAATAACAGAACTATTATCAGCTTAAATAACITTTTATATCTCAC 632
Sbjct 846 CTATTGGCATGGTATGGGATAATAGGACTATCATTAGCTTAAACAAGTATTATATCTCAC 905
Query 633 TATGCATTGTAAGAGGCCGGGAAATAAG 660
Sbjct 906 TATACATTGTAAGAGGCCAGGAAACAAG 933

```

Score = 370 bits (200), Expect = 9e-99  
 Identities = 284/324 (87%), Gaps = 8/324 (2%)  
 Strand=Plus/Plus

```

Query 8 GTAGTAAGAATCAACTGC-TGATTGCTA--TTGTACTAGCTAGTGCITACCTAACACATT 64
Sbjct 5 GTAGTAGGAATCTACTACTTGG-TTGGCAGCTTG--CTAGCTAGTATTGCTTAAATATATT 61
Query 65 GCAAGCAATTGTGACTGTTTTCTATGGCATAACCCGCTGGAGGAATGCATCCATTCCCC 124
Sbjct 62 GCACCCAGTATGTGACTGTTTTCTATGGCGTGCCCGCATGGAGAAATGCATCCATTCCCC 121
Query 125 TGTITTTGTGCAACCAAAAATAGAGATACTTGGGGAACGTACAGTGTCTGCCAGACAATG 184
Sbjct 122 TCTTCTGTGCAACTAAAAATAGAGATACTTGGGGAACCATACAGTGTCTGCCAGACAATG 181
Query 185 ATGATTATCAGGAAATAGCTTTAAATGTAACAGAGGC-TTTCGATGCATGGGATAATACA 243
Sbjct 182 ATGATTATCAGGAAATAGCTTTGAATGTGCAGAGGCCCTTT-GACGATGGGATAATACA 240
Query 244 GTAACAGAAACAGCAGTGGAGGATGCTCGGAATCTATTGAGACATCAATAAAACCATGT 303
Sbjct 241 GTAACAGAAACAGCAGTGGAAAGATGCTCGGAGTCTATTGAGACATCAATAAAACCATGC 300
Query 304 GTCAAATTAAACCCCTTATGTGTA 327
Sbjct 301 GTCAAAGTGACACCCCTTATGTGTA 324

```

>gb|AY509259.1| HIV-2 isolate MCN13, complete genome  
 Length=9713

Sort alignments for this  
 E value Score Percent  
 Query start position

Score = 593 bits (321), Expect = 5e-166  
 Identities = 463/528 (87%), Gaps = 23/528 (4%)  
 Strand=Plus/Plus

```

Query 672 ACCCAGGCAAGCATGGTGTGGTTCAAAGGCGAATGGAAGGAAGCCATGCGAGAGGTGAA 731
Sbjct 7132 ACCCAGACAAAGCATGGTGTGGTTCAAAGGTGAATGGAAGGAGGCCATGCGAGAGGTGAA 7191
Query 732 GGAGACCCCTTGCAGAAACATCCAGATATAAAGGGAA-C-AGGAGCCGCACAGAGAATATT 789
Sbjct 7192 GGAAGACCCCTTGCAGAAACATCCAGGTATAAA-GGAACCAATGA----AACAAAGAAATATT 7246
Query 790 AAATTTAAGCACCAGG-AAGAGGCTCAGACCCAGAAAGCAGCATACTGTGGACTAACTG 848
Sbjct 7247 AACTTTACAGCACCAGGAAAG-GGCTCAGACCCAGAGGTGGCATACTGTGGACTAACTG 7305
Query 849 CAGAGGGGAATTTCTCTACTGCGACATGACTTGGTTCCCTCAATTGGGTAGATAACAGGAC 908
Sbjct 7306 CAGAGGAGAATTTCTCTACTGCAACATGACTTGGTTCCCTCAATTGGATAG--AA-A--A- 7359
Query 909 GGGTCAGAAACAGCGCAATTATGCACCGTGCCATATAAGACAAAATAATTAATCTTGGCA 968
Sbjct 7360 ---TAAGACACACCGCAATTATGTACCGTGCCATATAAGACAAAATAATTAACACCTGGCA 7416
Query 969 CAGGGTAGGGAAAAACGTATATTTGCCCTCCAGGGAAGGGGAGTTGACCTGCAACTCAAC 1028
Sbjct 7417 TAAGGTAGGGAAAAATGTATATTTGCCCTCCAGGGAAGGGGAGTTGACCTGCAACTCAAC 7476
Query 1029 AGTGACCAGCATAATTGCCAACATTGATACG---GGAGATCAA-ACAGATATTACCTTTA 1084

```

```

Sbjct 7477 AGTAAC TAGCATAATTGCTAACATTGATGCAAAATGGAAAT-AATACAAATATTACCTTTA 7535
Query 1085 GTGCAGAGGTGGCAGAACTATACCGATTGGAATTTGGGAGATTACAATATTAGTAGAAATCA 1144
Sbjct 7536 GTGCAGAGGTGGCAGAACTATACCGATTAGAGTTGGGAGATTATAAATTGGTAGAAATAA 7595
Query 1145 CACCAATTGGCTTCGCACCTACATCAGTAAAGAGATACTCCTCTGCTC 1192
Sbjct 7596 CACCAATTGGCTTCGCACCTACAGCAGAAAAAGATACTCCTCTACTC 7643

```

Score = 479 bits (259), Expect = 1e-131  
 Identities = 303/325 (93%), Gaps = 0/325 (0%)  
 Strand=Plus/Plus

```

Query 336 CCATTGCAATACATCAGTCATCAAAGAGTCATGTGATAAGCACTATTGGGATGCTATGAG 395
Sbjct 6742 CCATTGCAACACATCGGTTCATCACAGAGTCATGTGACAAGCACTATTGGGATGCTATGAG 6801
Query 396 GTTTAGATACTGTGCACCACCGGGTTTGGCCCTACTAAGATGCAATGATATTAATTATC 455
Sbjct 6802 GTTTAGATACTGTGCACCACCGGGTTTGGCCCTACTAAGATGCAATGATACCAATTATC 6861
Query 456 AGGCTTTGCACTTAATTGCTCTAAAGTAGTAGCTGCTACATGCACCAAGATGATGGAAAC 515
Sbjct 6862 AGGCTTTGCGCCCAATTGCTCTAAAGTAGTAGCTGCTACATGCACCAAGATGATGGAAAC 6921
Query 516 GCAATCTTCTACATGGTTTGGCTTTAATGGCACTAGAACAGAAAAATAGAACATATATCTA 575
Sbjct 6922 GCAAACTTCTACATGGTTTGGCTTTAATGGCACTAGAACAGAAAAATAGAACATTTATCTA 6981
Query 576 TTGGCATGGTAAAAATAACAGAACTATTATCAGCTTAAATAACTTTTATAATCTCACTAT 635
Sbjct 6982 TTGGCATGGTAGGGATAACAGAACTATCATCAGCTTAAACAAATATTATAATCTCACTAT 7041
Query 636 GCATTGTAAGAGGCCGGGAAATAAG 660
Sbjct 7042 ACATTGTAAGAGGCCAGGAAATAAG 7066

```

Score = 412 bits (223), Expect = 1e-111  
 Identities = 296/331 (89%), Gaps = 6/331 (1%)  
 Strand=Plus/Plus

```

Query 1 ATGAAGGGTAGTAAG-AATCAACTGC-IGATTGCTATTGTACTAGCTAGTGCCTACCTAA 58
Sbjct 6146 ATGATGGGTGGT-AGAAATCAGCTGCTTG-TTGCCATTTTGTACTAGTACTTGCCTGA 6203
Query 59 CACATTGCAAGCAATT-TGTGACTGTTTTCTATGGCATACCCGCGTGGAGGAATGCATCC 117
Sbjct 6204 TATATTGC-ACCAATTATGTGACTGTTTTCTATGGCATACCCGCGTGGAGGAATGCATCC 6262
Query 118 ATTCCCTCTGTTTGTGCAACCAAAAATAGAGATACTTGGGGAACGTGACAGTGCCTGCCA 177
Sbjct 6263 ATTCCCTCTGTTTGTGCAACCAAGAAATAGGGATACTTGGGGAACCATACAGTGCCTGCCA 6322
Query 178 GACAATGATGATTATCAGGAAATAGCTTTAAATGTAAACAGAGGCTTTCGATGCATGGGAT 237
Sbjct 6323 GACAATGATGATTATCAGGAGATAACTTGAATGTGACAGAGGCTTTCGATGCATGGGAT 6382
Query 238 AATACAGTAACAGAACAGCAGTGGAGGATGTCTGGAACTATTGAGACATCAATAAAA 297
Sbjct 6383 AATACAGTAACAGAACAGCAATAGAAGATGTCTGGAACTATTGAGACATCAATAAAA 6442
Query 298 CCAATGTGTCAAATTAACACCCCTTATGTGTAG 328
Sbjct 6443 CCAATGTGTCAAATTAACGCCCTTATGTGTAG 6473

```

>emb|AJ001162.1|HIJ001162 Human Immunodeficiency Virus Type 2 partial envelope s  
 isolate sar from child in vertical transmission case  
 Length=1137

Sort alignments for this  
 E value Score Percen

Query start position

Score = 590 bits (319), Expect = 6e-165  
 Identities = 477/551 (86%), Gaps = 20/551 (3%)  
 Strand=Plus/Plus

Query	672	ACCCAGGCAAGCATGGTGTGGTTCAAAGGCGAATGGAAGGAAGCCATGCAGGAGGTGAA	731
Sbjct	575	ACCTAGGCAAGCATGGTGTGGTTTCAGAGGCAAATGGAAGGAAGCCATGCAGGAGGTGAA	634
Query	732	GGAGACCCCTTGCAGAAACATCCAGATATAAAGGGAAC-AGGAGCCGCA-CAGAGAATATT	789
Sbjct	635	GGAAACCCCTTGCAGAAACATCCAGGTATAAAGG-AACCACTAACA-CAAC-GA-AA-ATT	689
Query	790	AAATTTAAAGCACCAGGAAGAGGCTCAGACCCAGAAGCAGCATACATGTGGACTAAGTGC	849
Sbjct	690	AACCTTTACGGCACCAGGAAAGGCTCAGACCCAGAAGTAGAATACATGTGGACTAAGTGC	749
Query	850	AGAGGGGAATTTCTCTACTGCGCATGACTTGGTTCCTCAATTGGGTAGATAACAGGAC-	908
Sbjct	750	AGAGGAGAATTTCTCTACTGCAACATGAAATGGTTCCTCAATTGGATAGAAAACAAACT	809
Query	909	G-----GGTCAGAAACAGCGCAATTATGACCCGTGCCATATAAGACAAATAATTAATACT	963
Sbjct	810	GCATCAGGTGAGAAATGGCACAAATTATGTACCGTGCCATATAAGACAGATAGTTAACACC	869
Query	964	TGGCAGAGGTTAGGAAAAACGTATATTTGCCCTCCAGGGAAGGGGAGTTGACCTGCAAC	1023
Sbjct	870	TGGCATAAGGTTAGGAAAAATGTATATTTGCCCTCTAGGGAAGGAGAGTTAACCTGCAAC	929
Query	1024	TCAACAGTGACCAGCATAATTGCCAACATTGATACGGG-A-GA-TCAACAGATATTACC	1080
Sbjct	930	TCAACGGTGACCAGCATAATTGCCAACATTGAGATGACTAAGAATCAACAAATATTACC	989
Query	1081	TTTAGTGCAGAGGTGGCAGAACTATACCGATTGGAATTGGGAGATTACAAATTAGTAGAA	1140
Sbjct	990	TTTAGTGCAGAAAGTGGCAGAACTATACCGATTAGAATTGGGGGATTATAAATTGGTAGAA	1049
Query	1141	ATCACACCAATTTGGCT-TCGCACCTACATCAGTAAAGAGATACCTCTGCTCACCAG-A	1198
Sbjct	1050	ATAACACCAATTG-CTGTGCACCTACAGCAGAAAAAGATACCTCTGCTCAC-AGGA	1107
Query	1199	GACATACAAGA 1209	
Sbjct	1108	GACATACAAGA 1118	

Score = 451 bits (244), Expect = 3e-123  
 Identities = 299/326 (91%), Gaps = 2/326 (0%)  
 Strand=Plus/Plus

Query	336	CCATTGCAATACATCAGTCATCAAAGAGTCATGTGATAAGCACTATTGGGATGCTATGAG	395
Sbjct	188	CCATTGCAACACATCAGTCGTACAGAAATCATGTGATGAGCACTATTGGGATGCTATGAG	247
Query	396	GTTTAGATACTGTGCACCACCGGGTTTTGCCCTACTAAGATGCAATGATATTAATTATTC	455
Sbjct	248	GTTTAGATACTGTGCACCACCGGGTTTTGCCCTGCTAAGATGCAATGATACCAATTATTC	307
Query	456	AGGCTTTGCACCTAATTGCTCTAAAGTAGTAGCT-GCTACATGCACCAGAATGATGGAAA	514
Sbjct	308	AGGCTTTGAACCAATTGCTCTAAAGTAGTAGCTAG-TACCTGCACCAGAATGATGGAAA	366
Query	515	CGCAATCTTCTACATGGTTTGGCTTTAATGGCACTAGAACAGAAAAATAGAACATATATCT	574
Sbjct	367	CGCAAACTTCCACGTGGTCTGGCTTTAATGGCACTAGAGCAGAAAAATAGAACATATATCT	426
Query	575	ATTGGCATGGTAAAAATAACAGAACAATTATCAGCTTAAATAACITTTATAATCTCACTA	634
Sbjct	427	ATTGGCATGGTAGAGATAATAGAACTATAATCAGCTTAAACAAATATTATAATCTCACTT	486
Query	635	TGCATTGTAAGAGGCCGGGAAATAAG 660	
Sbjct	487	TGCATTGTAAGAGGCCAGGAAATAAG 512	

>gb|AY509260.1| HIV-2 isolate MCR35, complete genome  
Length=9588

Sort alignments for this  
E value Score Percen  
Query start position

Score = 588 bits (318), Expect = 2e-164  
Identities = 462/528 (87%), Gaps = 23/528 (4%)  
Strand=Plus/Plus

Query	672	ACCCAGGCAAGCATGGTGTGGTTCAAAGGCGAATGGAAGGAAGCCATGCAGGAGGTGAA	731
Sbjct	7132	ACCCAGACAGCAAGCATGGTGTGGTTCAAAGGTGAATGGAAGGGAGCCATGCAGGAGGTGAA	7191
Query	732	GGAGACCCCTTGCAGAACATCCAGATATAAAGGGA-C-AGGAGCCGCACAGAGAATATT	789
Sbjct	7192	GGAAACCCCTTGCAGAACATCCAGGTATAAA-GGAACCAATGA-----AACAAAGATATT	7246
Query	790	AAATTTAAAGCACCAGG-AAGAGGCTCAGACCCAGAAGCAGCATACATGTGGACTAACTG	848
Sbjct	7247	AACITTTACAGACACCAGGAAAG-GGCTCAGACCCAGAGGTGGCATAATGTGGACTAACTG	7305
Query	849	CAGAGGGGAATTTCTCTACTGCGACATGACTTGGTTCCTCAATTGGGTAGATAACAGGAC	908
Sbjct	7306	CAGAGGAGAATTTCTCTACTGCAACATGACTTGGTTCCTCAATTGGATAG--AA-A--A-	7359
Query	909	GGGTCAGAAACAGCGCAATTATGCACCGTGCCATATAAGACAATAAATAACTTGGCA	968
Sbjct	7360	---TAAGACACACCGCAATTATGTACCGTGCCATATAAAACAATAAATAACACTTGGCA	7416
Query	969	CAGGGTAGGGAAAAACGTATATTTGCCTCCCAGGGAAGGGGAGTTGACCTGCAACTCAAC	1028
Sbjct	7417	TAAGGTAGGGAAAAATGTATATTTGCCTCCCAGGGAAGGGGAGTTGACCTGCAACTCAAC	7476
Query	1029	AGTGACCAGCATAAATTGCCAACATTGATACGG--GAGA-TCAA-ACAGATATTACCTTTA	1084
Sbjct	7477	AGTAACATAGCATAAATTGCTAACATTGATGCAAAATGAAAAA-AAACAGATATTACCTTTA	7535
Query	1085	GTGCAGAGGTGGCAGAACTATACCGATTGGAATTGGGAGATTACAAATTAGTAGAAATCA	1144
Sbjct	7536	GTGCAGAGGTGGCAGAACTATACCGATTAGAGTTGGGAGATTATAAATTGGTAGAAATAA	7595
Query	1145	CACCAATTGGCTTCGCACCTACATCAGTAAAGAGATACCTCTCGCTC	1192
Sbjct	7596	CACCAATTGGCTTCGCACCTACAGCAGAAAAAGATACCTCTCTACTC	7643

Score = 479 bits (259), Expect = 1e-131  
Identities = 303/325 (93%), Gaps = 0/325 (0%)  
Strand=Plus/Plus

Query	336	CCATTGCAATACATCAGTCATCAAAGAGTCATGTGATAAGCACTATTGGGATGCTATGAG	395
Sbjct	6742	CCATTGCAACACATCCGTCATTACAGAGTCATGTGACAGAGCACTATTGGGATGCTATGAG	6801
Query	396	GTTTAGATACTGTGCACCACCGGGTTTGGCCCTACTAAGATGCAATGATATTAATTATTC	455
Sbjct	6802	GTTTAGATACTGTGCACCACCGGGTTTGGCCCTACTAAGATGCAATGATACCAATTATTC	6861
Query	456	AGGCTTTGCACCTAATTGCTCTAAAGTAGTAGCTGCTACATGCACAGAAATGATGGAAC	515
Sbjct	6862	AGGCTTTGCGCCCAATTGCTCTAAGTAGTAGCTGCTACATGCACAGAAATGATGGAAC	6921
Query	516	GCAATCTTCTACATGGTTTGGCTTTAATGGCACTAGAACAGAAAAATAGAACATATATCTA	575
Sbjct	6922	GCAAACTTCTACATGGTTTGGCTTTAATGGCACTAGAGCAGAAAAATAGAACATTTATCTA	6981
Query	576	TTGGCATGGTAAAAATAACAGAACTATTATCAGCTTAAATAACTTTTATAATCTCACTAT	635
Sbjct	6982	TTGGCATGGTAGGGATAACAGAACTATCATCAGCTTAAACAAGTATTATAATCTCACTAT	7041
Query	636	GCATTGTAAGAGGCCGGGAAATAAG	660
Sbjct	7042	ACATTGTAAGAGGCCAGGAAATAAG	7066